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OM protein - protein search, using sw model

Run on: March 18, 2005, 15:03:42 ; Search time 169 Seconds  
(without alignments)  
1096.202 Million cell updates/sec

Title: US-10-798-773-2  
Perfect score: 2500  
Sequence: 1 MDATIAPIRIPPEMPQYGE.....YTFEYIESGIINLPKIP 479

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq 16Dec04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003s:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2500	100.0	479	ABB82701	Abb82701 Novel hum
2	2500	100.0	479	ADA55452	Ada55452 Human pro
3	2500	100.0	479	Aae34860	Aae34860 Human kin
4	2484	99.4	491	ADC10110	ADC10110 Human NOV
5	2248	89.9	510	ADC10108	ADC10108 Human NOV
6	1571	62.8	571	AAM38895	Aam38895 Human pol
7	1429	57.2	275	AAE16279	Aae16279 Human kin
8	1429	57.2	275	ADB65473	Adb65473 Human pro
9	1301	52.0	258	AAE07843	Aae07843 Human 278
10	1301	52.0	258	ABW00581	Abw00581 Human 278
11	1184.5	47.4	240	AAM40681	Aam40681 Human pol
12	1166	46.6	236	ADB94013	Adb94013 Human nov
13	1166	46.6	236	ADB94013	Adb94013 Human nov
14	806	32.2	226	AM78417	Aam78417 Human pro
15	806	32.0	226	AM78401	Aam78401 Human pro
16	648	25.9	125	AGS59945	Agb59945 Human DIT
17	553	22.1	113	AAU17614	Aau17614 Novel sig
18	553	22.1	113	AAU17303	Aau17303 Novel sig
19	553	22.1	113	AAW85250	Aam85250 Human imm
20	553	22.1	113	ADB94322	Adb94322 Human nov
21	553	22.1	113	ADB94011	Adb94011 Human nov
22	491	19.6	94	ABB82702	Abb82702 Novel hum
23	364.5	14.6	283	5 ABB93735	Abb93735 Herbicida
24	364.5	14.6	283	8 ADN74247	Adn74247 Thale cre
25	281	11.2	212	6 ABU44285	Abu44285 Protein e

## RESULT 1

ABB82701  
ID ABB82701 standard; protein; 479 AA.

AC ABB82701;

DT 07-MAR-2003 (first entry)

DE Novel human kinase polypeptide (NHP).

KW NHP; kinase; gene therapy; drug screening; human; enzyme.

OS Homo sapiens.

PN WO200290517-A2.

PD 14-NOV-2002.

PF 08-MAY-2002; 2002WO-US014669.

PR 09-MAY-2001; 2001US-0289727P.

XX (LEXI-) LEXICON GENETICS INC.

XX Yu X, Xie Q, Abuin A, Walke DW;

XX WPI; 2003-103514/09.

XX N-PSDB; ABV75301.

XX New human kinase proteins and polynucleotides, useful for cosmetic and nutraceutical applications, drug screening, clinical trial monitoring, diagnosing or treating diseases associated with biological disorders or imbalances.

XX Claim 3; Page 38-39; 40pp; English.

XX The invention relates to novel human polypeptides (NHP) having kinase activity and polynucleotides encoding them. The polynucleotides, proteins, antibodies, agonists and antagonists of the proteins are useful for drug screening, clinical trial monitoring, and diagnosing or treating diseases or disorders associated with biological disorders or imbalances. The proteins and polynucleotides are useful in cosmetic and nutraceutical applications, for identifying protein coding sequences and mapping a unique gene to a particular chromosome. The sequences of the polynucleotides and proteins can also be used as additional DNA markers for restriction fragment length polymorphism analysis, or in forensic biology. The present sequence represents a NHP kinase

## ALIGNMENTS

26	280.5	11.2	222	6	ADA34388
27	278.5	11.1	217	6	ABU16970
28	273	10.9	212	6	ABU00572
29	273	10.9	212	6	ABP81534
30	273	10.9	212	8	ADK47609
31	273	10.9	216	8	ADR96130
32	272	10.9	212	4	AAU37626
33	272	10.9	212	6	ABU45820
34	271	10.8	220	6	ABU22212
35	261	10.4	212	5	ABP29896
36	261	10.4	212	8	ADK99153
37	260.5	10.4	212	6	ABU20277
38	260	10.4	215	6	ABU24095
39	259	10.4	212	5	ABF28573
40	259	10.4	212	6	ABU46412
41	258	10.3	211	8	ADK98859
42	258	10.3	211	8	ADK99154
43	258	10.3	212	5	ABP28572
44	257.5	10.3	214	6	ABU49276
45	257	10.3	207	8	ADK98866

SQ Sequence 479 AA;

Query Match 100.0%; Score 2500; DB 6; Length 479;  
Best Local Similarity 100.0%; Pred. No. 5.1e-234;  
Matches 479; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDATIAPIRPPMPQYGEENHIFELMOMLEQLLIHQPEDPFPFMIQHLHRDNDNVPI 60  
DB 1 MDATIAPIRPPMPQYGEENHIFELMOMLEQLLIHQPEDPFPFMIQHLHRDNDNVPI 60  
QY 61 VILGPPASGKTTIAMWLCKHNSLLTLENILNEFSYATARRLYLQKTVPSALLVQ 120  
DB 61 VILGPPASGKTTIAMWLCKHNSLLTLENILNEFSYATARRLYLQKTVPSALLVQ 120  
QY 121 LIQERLAEDDCIKQWILDGIPETREQALRIQTLGTPRHVIVLSAPDVTVLIERNLGKRI 180  
DB 121 LIQERLAEDDCIKQWILDGIPETREQALRIQTLGTPRHVIVLSAPDVTVLIERNLGKRI 180  
QY 181 DPQTGEIYHTTFDWPPESEIQNRLMVPEDISELETAQKLEYHRNIVRVIPSPKILKVI 240  
DB 181 DPQTGEIYHTTFDWPPESEIQNRLMVPEDISELETAQKLEYHRNIVRVIPSPKILKVI 240  
QY 241 SADQPCVDVYQALTYVQSNHRTNAPFTPRVLLGLPGVSGSKSLQAALLAQKYLNVNCCG 300  
DB 241 SADQPCVDVYQALTYVQSNHRTNAPFTPRVLLGLPGVSGSKSLQAALLAQKYLNVNCCG 300  
QY 301 QLLKEAVADRTTFGELIQPFPEKEMAVPDSLLMKVLSQRLDQDCIQKGMVLHGVRDL 360  
DB 301 QLLKEAVADRTTFGELIQPFPEKEMAVPDSLLMKVLSQRLDQDCIQKGMVLHGVRDL 360  
QY 361 QAHLNRLGYNPNRVFFLNVPFDSIMERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQ 420  
DB 361 QAHLNRLGYNPNRVFFLNVPFDSIMERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQ 420  
QY 421 NPKDAEQVKLMDLFYRNSADLEQLYGSATLNGDQDPYTFVEYIESGIINPLPKKIP 479  
DB 421 NPKDAEQVKLMDLFYRNSADLEQLYGSATLNGDQDPYTFVEYIESGIINPLPKKIP 479

RESULT 2  
ADA55452 standard; protein; 479 AA.

XX ADA55452;  
AC ADA55452;  
XX 20-NOV-2003 (first entry)  
DT Human protein, SEQ ID 3020.  
DE Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;  
KW Gene therapy; human; secretory protein; membrane proteins; cancer;  
KW inflammatory disease; osteoporosis; neurological disease.  
XX Homo sapiens.  
OS EP1293569-A2.  
XX 19-MAR-2003.  
XX 21-MAR-2002; 2002EP-00006586.  
XX 14-SEP-2001; 2001JP-00328381.  
XX 24-JAN-2002; 2002US-0350435P.  
XX (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX Isogai T, Sugiyama T, Otsuka T, Wakamatsu A, Sato H, Iehli S;  
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;  
XX WPI; 2003-395539/38.  
DR N-PSDB; ADA53813.

XX New polynucleotides encoding full-length polypeptides, e.g. secretory  
PT and/or membrane proteins, useful for developing medicines for diseases in  
PT which the gene is involved, or as target molecules for gene therapy.  
XX Claim 14; SEQ ID NO 3020; 205pp; English.  
PS The present invention relates to novel human secretory or membrane  
CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-  
CC ADA54071). The coding sequences are useful in the gene therapy of  
CC diseases caused by abnormalities of the proteins, e.g. cancer,  
CC inflammatory diseases, osteoporosis or neurological disease.  
XX Sequence 479 AA;

Query Match 100.0%; Score 2500; DB 6; Length 479;  
Best Local Similarity 100.0%; Pred. No. 5.1e-234;  
Matches 479; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDATIAPIRPPMPQYGEENHIFELMOMLEQLLIHQPEDPFPFMIQHLHRDNDNVPI 60  
DB 1 MDATIAPIRPPMPQYGEENHIFELMOMLEQLLIHQPEDPFPFMIQHLHRDNDNVPI 60  
QY 61 VILGPPASGKTTIAMWLCKHNSLLTLENILNEFSYATARRLYLQKTVPSALLVQ 120  
DB 61 VILGPPASGKTTIAMWLCKHNSLLTLENILNEFSYATARRLYLQKTVPSALLVQ 120  
QY 121 LIQERLAEDDCIKQWILDGIPETREQALRIQTLGTPRHVIVLSAPDVTVLIERNLGKRI 180  
DB 121 LIQERLAEDDCIKQWILDGIPETREQALRIQTLGTPRHVIVLSAPDVTVLIERNLGKRI 180  
QY 181 DPQTGEIYHTTFDWPPESEIQNRLMVPEDISELETAQKLEYHRNIVRVIPSPKILKVI 240  
DB 181 DPQTGEIYHTTFDWPPESEIQNRLMVPEDISELETAQKLEYHRNIVRVIPSPKILKVI 240  
QY 241 SADQPCVDVYQALTYVQSNHRTNAPFTPRVLLGLPGVSGSKSLQAALLAQKYLNVNCCG 300  
DB 241 SADQPCVDVYQALTYVQSNHRTNAPFTPRVLLGLPGVSGSKSLQAALLAQKYLNVNCCG 300  
QY 301 QLLKEAVADRTTFGELIQPFPEKEMAVPDSLLMKVLSQRLDQDCIQKGMVLHGVRDL 360  
DB 301 QLLKEAVADRTTFGELIQPFPEKEMAVPDSLLMKVLSQRLDQDCIQKGMVLHGVRDL 360  
QY 361 QAHLNRLGYNPNRVFFLNVPFDSIMERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQ 420  
DB 361 QAHLNRLGYNPNRVFFLNVPFDSIMERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQ 420  
QY 421 NPKDAEQVKLMDLFYRNSADLEQLYGSATLNGDQDPYTFVEYIESGIINPLPKKIP 479  
DB 421 NPKDAEQVKLMDLFYRNSADLEQLYGSATLNGDQDPYTFVEYIESGIINPLPKKIP 479

RESULT 3  
AAE34860 standard; protein; 479 AA.

XX AAE34860;  
AC AAE34860;  
XX 28-MAY-2003 (first entry)  
DT Human kinases and phosphatases (KPP)-3.  
DE Human; kinase and phosphatase; KPP; enzyme; cardiovascular disorder;  
KW neurological disorder; cancer; gene therapy.  
XX Homo sapiens.  
OS Key  
XX Binding-site 64..71 Location/Qualifiers  
FT Binding-site /note= "ATP/GTP binding site motif A (P-loop)"  
FT Binding-site 275..282 /note= "ATP/GTP binding site motif A (P-loop)"  
FT Binding-site /note= "ATP/GTP binding site motif A (P-loop)"  
XX

PN WO200294780-A2.  
XX 28-NOV-2002.  
PD 23-MAY-2002; 2002WO-US016634.  
XX 24-MAY-2001; 2001US-0293665P.  
XX 15-JUN-2001; 2001US-0298712P.  
PR 06-JUL-2001; 2001US-0303418P.  
PR 19-JUL-2001; 2001US-0306967P.  
PR 27-JUL-2001; 2001US-0308183P.  
PR 19-DEC-2001; 2001US-0343007P.  
PR 15-FEB-2002; 2002US-0357675P.  
PR 30-APR-2002; 2002US-0376988P.  
XX (INCY-) INCYTE GENOMICS INC.  
PA Yue H, Lu DM, Azimzai Y, Ding L, Lee EA, Hafalia AJA, Becha SD;  
XX Tang Y, Lal PG, Griffin JA, Gururajan R, Ramkumar J, Elliott VS;  
PI Arvizu CS, Luo W, Swarnakar A, Duggan BM, Tran UK, Walia NK;  
PI Gandhi AR, Yao MG, Khan FA, Baughn MR, Borowsky ML, Zebazadian Y;  
PI Richardson TW, Marquis JP, Chien D, Jin P;  
XX WPI; 2003-120774/11.  
DR N-PSDB; AAD53173.  
XX New human kinases and phosphatases (KPP), useful for preparing a  
PT composition for diagnosing or treating a disease or condition associated  
PT with decreased expression or overexpression of functional KPP e.g.,  
PT cancer.  
XX Claim 1; Col 133-134; 82pp; English.  
XX The invention relates to novel human kinases and phosphatases (KPP)  
CC polypeptides and polynucleotides. Polypeptides of the invention are used  
CC for screening agonists and antagonists. They are used to make monoclonal  
CC or polyclonal or antibodies, which are used in diagnostic tests for  
CC conditions or diseases associated with expression of the polypeptide.  
CC They are also useful for diagnosing or treating diseases or conditions  
CC associated with decreased expression or overexpression of functional KPP  
CC e.g. cardiovascular or neurological disorders or cancer. The invention is  
CC useful in gene therapy. The present sequence is human KPP protein  
XX Sequence 479 AA;  
SQ  
Query Match 100.0%; Score 2500; DB 6; Length 479;  
Best Local Similarity 100.0%; Pred. No. 5.1e-234;  
Matches 479; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDATTAPRIPPMPQYGEENHIFELMQNMLEQLLIHQPEDPIPFMIQHLHRDNDNVPI 60  
DB 1 MDATTAPRIPPMPQYGEENHIFELMQNMLEQLLIHQPEDPIPFMIQHLHRDNDNVPI 60  
QY 61 VILGPPASGKTTIAMWCKHNSLLTLENILNFSYTTATARRLYLQKTVPSALLVQ 120  
DB 61 VILGPPASGKTTIAMWCKHNSLLTLENILNFSYTTATARRLYLQKTVPSALLVQ 120  
QY 121 LIQRLAEDCIKQWILGIDIPETREQALRIQTIGITPRHIVLSAPDVLIERNLGRI 180  
DB 121 LIQRLAEDCIKQWILGIDIPETREQALRIQTIGITPRHIVLSAPDVLIERNLGRI 180  
QY 181 DPQTGEYHTFDWPPESIQNRLMVPDISELTAQKLEYHRNIVRVIPYKILKVI 240  
DB 181 DPQTGEYHTFDWPPESIQNRLMVPDISELTAQKLEYHRNIVRVIPYKILKVI 240  
QY 241 SADQPCVDVYQALTVVQSNHRTNAPFTPRVLLGPGVSGSKSQALLAQKRLVNVCCG 300  
DB 241 SADQPCVDVYQALTVVQSNHRTNAPFTPRVLLGPGVSGSKSQALLAQKRLVNVCCG 300  
QY 301 QLLKEAVADRTTFGELLIPPEKEMAVPDSLLMKVLSQRLDQDDCIQKGNVLHGVRDL 360  
DB 301 QLLKEAVADRTTFGELLIPPEKEMAVPDSLLMKVLSQRLDQDDCIQKGNVLHGVRDL 360

QY 361 QAHLLNRLGYNPNRVFFLNVPFDSIMERLTLLRIDPVTGERYHLMYKPPPTMEIQARLLQ 420  
DB 361 QAHLLNRLGYNPNRVFFLNVPFDSIMERLTLLRIDPVTGERYHLMYKPPPTMEIQARLLQ 420  
QY 421 NPKDAEQQVKLQMDLFYRNSADLEQLYGSAITLNGDQDPYTVFYEISGIIINPLPKKIP 479  
DB 421 NPKDAEQQVKLQMDLFYRNSADLEQLYGSAITLNGDQDPYTVFYEISGIIINPLPKKIP 479

RESULT 4  
ADC10110  
ID ADC10110 standard; protein; 491 AA.  
XX AC ADC10110;  
XX DT 18-DEC-2003 (first entry)  
XX Human NOVX polypeptide SEQ ID NO: 130.  
XX cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective;  
KW antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX;  
KW pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder;  
KW inflammatory disorder; chromosome mapping; tissue typing;  
KW predictive medicine.  
XX OS Homo sapiens.  
XX PN WO2003000842-A2.  
XX PD 03-JAN-2003.  
XX PF 04-JUN-2002; 2002WO-US017443.  
XX 04-JUN-2001; 2001US-0295607P.  
PR 04-JUN-2001; 2001US-0295661P.  
PR 06-JUN-2001; 2001US-0296404P.  
PR 06-JUN-2001; 2001US-0296418P.  
PR 07-JUN-2001; 2001US-0296575P.  
PR 11-JUN-2001; 2001US-0297414P.  
PR 12-JUN-2001; 2001US-0295573P.  
PR 12-JUN-2001; 2001US-0297567P.  
PR 14-JUN-2001; 2001US-0298285P.  
PR 15-JUN-2001; 2001US-0298528P.  
PR 18-JUN-2001; 2001US-0299133P.  
PR 19-JUN-2001; 2001US-0299230P.  
PR 21-JUN-2001; 2001US-0299949P.  
PR 22-JUN-2001; 2001US-0300177P.  
PR 26-JUN-2001; 2001US-0300883P.  
PR 28-JUN-2001; 2001US-0301530P.  
PR 28-JUN-2001; 2001US-0301550P.  
PR 03-JUL-2001; 2001US-0302951P.  
PR 31-JUL-2001; 2001US-0308890P.  
PR 14-SEP-2001; 2001US-032297P.  
PR 25-SEP-2001; 2001US-0324669P.  
PR 03-DEC-2001; 2001US-0337477P.  
PR 14-DEC-2001; 2001US-0341562P.  
PR 21-FEB-2002; 2002US-0358568P.  
PR 22-FEB-2002; 2002US-0359122P.  
PR 22-FEB-2002; 2002US-035978P.  
PR 22-FEB-2002; 2002US-0359034P.  
PR 22-FEB-2002; 2002US-0359035P.  
PR 22-FEB-2002; 2002US-0359121P.  
PR 27-FEB-2002; 2002US-0359964P.  
PR 01-MAR-2002; 2002US-0360858P.  
PR 12-MAR-2002; 2002US-0363430P.  
PR 12-MAR-2002; 2002US-0363676P.  
PR 10-APR-2002; 2002US-0371346P.  
PR 10-MAY-2002; 2002US-0379444P.  
PR 04-JUN-2002; 2002US-00379444.  
XX (CUBA-) CURAGEN CORP.  
XX Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;  
PI

PI Dippio VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;  
 PI Gerlach VL, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W, Kekuda R;  
 PI Kramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;  
 PI Ort T, Padigar M, Patturajan M, Pena CE, Rastelli L, Rieger DK;  
 PI Rothenberg ME, Shenoy SG, Shinkets RA, Smithson G, Spaderma SK;  
 PI Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;  
 PI Burgess CE, Lepley DM;  
 XX WPI; 2003-210149/20.  
 DR N-PSDB; ADC10109.  
 XX New isolated NOVX polypeptides and nucleic acid molecules useful for  
 PT treating, preventing and diagnosing pathological conditions with NOVX-  
 PT associated disorders, such as cancer, obesity, diabetes and inflammatory  
 PT or CNS diseases.  
 XX Claim 1; SEQ ID NO 130; 772pp; English.  
 XX The invention relates to novel isolated polypeptides, mature form of the  
 CC polypeptide, a sequence that is 95% identical to the polypeptide or the  
 CC polypeptide comprising one or more conservative substitutions. The NOVX  
 CC polypeptide is useful for treating or preventing a pathology associated  
 CC with the polypeptide e.g. disorders associated with aberrant expression  
 CC or activity of the polypeptide, such as cancer, diabetes, obesity, and  
 CC endocrine, CNS and inflammatory disorders. They can also be used in  
 CC various detection and screening assays, chromosome mapping, tissue typing  
 CC and predictive medicine. This sequence corresponds to one of the  
 CC polypeptides of the invention.  
 XX Sequence 491 AA;

Query Match 99.4%; Score 2484; DB 7; Length 491;  
 Best Local Similarity 97.6%; Pred. No. 1.9e-232;  
 Matches 479; Conservative 0; Mismatches 0; Indels 12; Gaps 1;  
 N-PSDB; ADC10109.  
 QY 1 MDATIAHPRIPEMPQGEENHIFELM-----QNMLEQLLIHQEPDIPPMIQ 48  
 DB 1 MDATIAHPRIPEMPQGEENHIFELMQVLTWVSALHPQNMLEQLLIHQEPDIPPMIQ 60  
 QY 49 HLHRDNDNPRVILGPPASGKTTIAMWLCKHNSLLTLENILNEFSYTATEARLYL 108  
 DB 61 HLHRDNDNPRVILGPPASGKTTIAMWLCKHNSLLTLENILNEFSYTATEARLYL 120  
 QY 109 QRKTVPSALLVQLIOERLAEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPD 168  
 DB 121 QRKTVPSALLVQLIOERLAEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPD 180  
 QY 169 TVLIERNLGRKIDPOTGEIYHTTFDWPPESEIQNRLMVPEDISELETAQKLLEYHRNIVR 228  
 DB 181 TVLIERNLGRKIDPOTGEIYHTTFDWPPESEIQNRLMVPEDISELETAQKLLEYHRNIVR 240  
 QY 229 VIPSPKILKVISADQPCVDVYQALTYVQSNHRTNAPFTPRVLLGVPVSGSKSLQAALL 288  
 DB 241 VIPSPKILKVISADQPCVDVYQALTYVQSNHRTNAPFTPRVLLGVPVSGSKSLQAALL 300  
 QY 289 AQKRLNVNCGQLLKXAVADRTTFGELIQPFPEKEMAVPDSLLMKVLSORLDDQDCIQK 348  
 DB 301 AQKRLNVNCGQLLKXAVADRTTFGELIQPFPEKEMAVPDSLLMKVLSORLDDQDCIQK 360  
 QY 349 GWWLHGVRDLDQAHLLNRLGYNRNVFFLNVPPDSIMERLTARRIDPVTGERVHLMYKP 408  
 DB 361 GWWLHGVRDLDQAHLLNRLGYNRNVFFLNVPPDSIMERLTARRIDPVTGERVHLMYKP 420  
 QY 409 PPTWEIQARLQNPDAEEQVKLQNDLFYRNSADLEQLYGSAILTNGDQDPYTVFYEIES 468  
 DB 421 PPTWEIQARLQNPDAEEQVKLQNDLFYRNSADLEQLYGSAILTNGDQDPYTVFYEIES 480  
 QY 469 GIINPLPKKIP 479  
 DB 481 GIINPLPKKIP 491

ADCL0108  
 ID ADC10108 standard; protein; 510 AA.  
 AC  
 XX ADC10108;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 XX Human NOVX polypeptide SEQ ID NO: 128.  
 XX  
 XX cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective;  
 KW antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX;  
 KW pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder;  
 KW inflammatory disorder; chromosome mapping; tissue typing;  
 KW predictive medicine.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2003000842-A2.  
 XX  
 XX 03-JAN-2003.  
 XX  
 XX 04-JUN-2002; 2002WO-US017443.  
 XX  
 PR 04-JUN-2001; 2001US-0295607P.  
 PR 04-JUN-2001; 2001US-0295661P.  
 PR 06-JUN-2001; 2001US-0296404P.  
 PR 06-JUN-2001; 2001US-0296418P.  
 PR 07-JUN-2001; 2001US-0296575P.  
 PR 11-JUN-2001; 2001US-0297414P.  
 PR 12-JUN-2001; 2001US-0295573P.  
 PR 12-JUN-2001; 2001US-0297567P.  
 PR 14-JUN-2001; 2001US-0298285P.  
 PR 15-JUN-2001; 2001US-0298528P.  
 PR 18-JUN-2001; 2001US-0299133P.  
 PR 19-JUN-2001; 2001US-0299230P.  
 PR 21-JUN-2001; 2001US-0299949P.  
 PR 22-JUN-2001; 2001US-0300177P.  
 PR 26-JUN-2001; 2001US-0300883P.  
 PR 28-JUN-2001; 2001US-0301530P.  
 PR 28-JUN-2001; 2001US-0301550P.  
 PR 03-JUL-2001; 2001US-0302951P.  
 PR 31-JUL-2001; 2001US-0308890P.  
 PR 14-SEP-2001; 2001US-0322297P.  
 PR 25-SEP-2001; 2001US-0324669P.  
 PR 03-DEC-2001; 2001US-0337477P.  
 PR 14-DEC-2001; 2001US-0341562P.  
 PR 21-FEB-2002; 2002US-0358656P.  
 PR 21-FEB-2002; 2002US-0359122P.  
 PR 22-FEB-2002; 2002US-0359034P.  
 PR 22-FEB-2002; 2002US-0359035P.  
 PR 22-FEB-2002; 2002US-0359121P.  
 PR 27-FEB-2002; 2002US-0359964P.  
 PR 01-MAR-2002; 2002US-0360858P.  
 PR 12-MAR-2002; 2002US-0363430P.  
 PR 12-MAR-2002; 2002US-0363676P.  
 PR 10-APR-2002; 2002US-0371346P.  
 PR 10-MAY-2002; 2002US-0379444P.  
 PR 04-JUN-2002; 2002US-00379444.  
 (CURA-) CURAGEN CORP.  
 AGEE ML, Anderson DW, Berghs C, Casman SJ, Catterton E;  
 Dippio VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;  
 Gerlach VL, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W, Kekuda R;  
 Kramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;  
 Ort T, Padigar M, Patturajan M, Pena CE, Rastelli L, Rieger DK;  
 Rothenberg ME, Shenoy SG, Shinkets RA, Smithson G, Spaderma SK;  
 Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;  
 Burgess CE, Lepley DM;  
 WPI; 2003-210149/20.  
 N-PSDB; ADC10107.



XX New isolated NOVX polypeptides and nucleic acid molecules useful for  
PT treating, preventing and diagnosing pathological conditions with NOVX-  
PT associated disorders, such as cancer, obesity, diabetes and inflammatory  
PT or CNS diseases.  
XX  
PS Claim 1; SEQ ID NO 128; 772pp; English.  
XX  
XX The invention relates to novel isolated polypeptides, mature form of the  
CC polypeptide, a sequence that is 95% identical to the polypeptide or the  
CC polypeptide comprising one or more conservative substitutions. The NOVX  
CC polypeptide is useful for treating or preventing a pathology associated  
CC with the polypeptide e.g. disorders associated with aberrant expression  
CC or activity of the polypeptide, such as cancer, diabetes, obesity, and  
CC endocrine, CNS and inflammatory disorders. They can also be used in  
CC various detection and screening assays, chromosome mapping, tissue typing  
CC and predictive medicine. This sequence corresponds to one of the  
CC polypeptides of the invention.  
XX  
SQ Sequence 510 AA;

Query Match 89.9%; Score 2248; DB 7; Length 510;  
Best Local Similarity 90.8%; Pred. No. 1.9e-209;  
Matches 435; Conservative 0; Mismatches 0; Indels 44; Gaps 1;  
QY 1 MDATIAPIRPPMPQYGEENHIFELMQLNLEQLLIHQPDPIPFMIQHLHRDNDNVPRI 60  
DB 76 MDATIAPIRPPMPQYGEENHIFELMQLNLEQLLIHQPDPIPFMIQHLHRDNDNVPRI 135  
QY 61 VILGPASGKTTIAMWLCCKHNSLLTLENLILNEFSYTAARRLYLQKTVPSALLVQ 120  
DB 136 VILGPASGKTTIAMWLCCKHNSLLTLENLILNEFSYTAARRLYLQKTVPSALLVQ 195  
QY 121 LIQRLAEDDCIKQWILDGIPETREQALRIQTGLTPRHVIVLSAPDVTLLIERNLGRRI 180  
DB 196 LIQRLAEDDCIKQWILDGIPETREQALRIQTGLTPRHVIVLSAPDVTLLIERNLGRRI 255  
QY 181 DPOTGEIYHTFTFWPPESIQNRLMVPEDISELETAQKLEHYNIRVIPSYPKILKVI 240  
DB 256 DPOTGEIYHTFTFWPPESIQNRLMVPEDISELETAQKLEHYNIRVIPSYPKILKVI 315  
QY 241 SADQPCVDVFPYQALTYVQSNHRTNAPFTPRVLLGPGVSGSKQAALLAQKRLVNVCCG 300  
DB 316 SADQPCVDVFPYQALTYVQSNHRTNAPFTPRVLLGPGVSGSKQAALLAQKRLVNVCCG 375  
QY 301 QLLKEAVADRTTFGELIQPFPEKEMAVPDSLLMKVLSQRDQDCTQKGNVLHGVPRDL 360  
DB 376 QL-----QKGNVLHGVPRDL 391  
QY 361 QALLNLRLGYNPNRVFFLNVPDPSIMERLTLRRIDPVTGERYHMYKPPPTMEIQARLLQ 420  
DB 392 QALLNLRLGYNPNRVFFLNVPDPSIMERLTLRRIDPVTGERYHMYKPPPTMEIQARLLQ 451  
QY 421 NPKDAEQVKLQMDLFPYRNSADLEQYGSATLNGDDQDPTVTFEYESGILNPLPKKIP 479  
DB 452 NPKDAEQVKLQMDLFPYRNSADLEQYGSATLNGDDQDPTVTFEYESGILNPLPKKIP 510

RESULT 6  
AA038895  
ID AA038895 standard; protein; 571 AA.  
XX  
AC AA038895;  
XX  
DT 22-OCT-2001 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 2040.  
XX  
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

KW leukaemia.  
XX  
OS Homo sapiens.  
XX  
PN WO200153312-A1.  
XX  
XX 26-JUL-2001.  
XX  
XX 26-DEC-2000; 2000WO-US034263.  
XX  
XX 23-DEC-1999; 99US-00471275.  
PR 21-JAN-2000; 2000US-00486725.  
PR 25-APR-2000; 2000US-00552317.  
PR 20-JUN-2000; 2000US-00598042.  
PR 19-JUL-2000; 2000US-00620312.  
PR 03-AUG-2000; 2000US-00653450.  
PR 14-SEP-2000; 2000US-00662191.  
PR 19-OCT-2000; 2000US-00693036.  
PR 29-NOV-2000; 2000US-00727344.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
PI Zhou P, Goodrich R, Drmanac RT;  
XX  
XX WPI, 2001-442253/47.  
DR N-PSDB; AAI58051.  
XX  
XX Novel nucleic acids and polypeptides, useful for treating disorders such  
PT as central nervous system injuries.  
PT  
XX  
PS Example 3; SEQ ID NO 2040; 10078pp; English.  
XX  
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the  
CC encoded polypeptides (AAM38642-AAI62213) with nootropic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localised neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC activation of the activities such as: immune system suppression,  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemia and  
CC C.N.S disorders. Note: The sequence data for this patent did not form  
CC part of the printed specification  
XX  
SQ Sequence 571 AA;

Query Match 62.8%; Score 1571; DB 4; Length 571;  
Best Local Similarity 53.6%; Pred. No. 1.9e-143;  
Matches 336; Conservative 4; Mismatches 11; Indels 276; Gaps 4;  
QY 1 MDATIAPIRPPMPQYGEENHIFELMQLNLEQLLIHQPDPIPFMIQHLHRDNDNVPRI 60  
DB 1 MDATIAPIRPPMPQYGEENHIFELMQLNLEQLLIHQPDPIPFMIQHLHRDNDNVPRI 28  
QY 61 VILGPASGKTTIAMWLCCKHNSLLTLENLILNEFSYTAARRLYLQKTVPSALLVQ 120  
DB 29 -----AMWLCCKHNSLLTLENLILNEFSYTAARRLYLQKTVPSALLVQ 75  
QY 121 LIQRLAEDDCIKQWILDGIPETREQALRIQTGLTPRHVIVLSAPDVTLLIERNLGRRI 180  
DB 76 LIQRLAEDDCIKQWILDGIPETREQALRIQTGLTPRHVIVLSAPDVTLLIERNLGRRI 135  
QY 181 DPOTGEIYHTFTFWPPESIQNRLMVPEDISELETAQKLEHYNIRVIPSYPKILKVI 240  
DB 136 DPOTGEIYHTFTFWPPESIQNRLMVPEDISELETAQKLEHYNIRVIPSYPKILKVI 195  
QY 241 SADQPCVDVFPYQALTYVQSNHRTNAPFTPRVLLGPGVSGSKQAALLAQKRLVNVCCG 300

Db 196 SADQPCVDVYQALTYVQSHRTNAPFTPRVLLGPGVSGSKLQALLAQKYLNVNCCG 355  
QY 301 QLLKEAVADRTTGGELIQPFKEKA----- 326  
Db 256 QLLKEAVADRTTGGELIQPFKEKAEGGHRVKGTVFSPRTLPCNQKDLPCLLKLEDM 315  
QY 327 ----- 326  
Db 316 LYLRLSELPEELLVGLPVTGSELSQIPLFNPRPNRGRCILPLSLMEHPRLTGA 375  
QY 327 ----- 326  
Db 376 DTGSFSLGCGRLQRCQDMRGEEVAPVTLCSLYTYDQGSLLDGLGIGILQEGDRPGT 435  
QY 327 -----VPSLL 332  
Db 436 QGPOEKEKQMPASPMNTDAHLNDFKEGLKERSYTGQFPAVNRDDEERGCGGVVPSLL 495  
QY 333 MKVLSQRLDQDCIQKQWLVHGVPRDLQAHLLNRLGYNPNRVFLNVPFDSIMERLTLR 392  
Db 496 MKVLSQRLDQDCIQKQWLVHGVPRDLQAHLLNRLGYNPNRA----- 538  
QY 393 RIDPVTGERVHLMKPPPTMEIQARLL 419  
Db 539 ---QLKGSRLH---KPSRVPEVECLLV 559

RESULT 7  
AAE16279 standard; protein; 275 AA.

AC AAE16279;  
XX  
XX 26-MAR-2002 (first entry)  
DE Human kinase PKIN-25 protein.  
XX  
XX Human; kinase; PKIN-25; cancer; leukaemia; adenocarcinoma; osteoporosis;  
KW immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;  
KW Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;  
KW allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;  
KW autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis;  
KW Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;  
KW rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome;  
KW hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;  
KW cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;  
KW congestive heart failure; ischaemic heart disease; lung tumour; gout;  
KW fatty liver; Niemann-Pick's disease; gene therapy.  
XX  
OS Homo sapiens.  
XX  
XX WO200196547-A2.  
XX  
XX 20-DEC-2001.  
XX  
XX 14-JUN-2001; 2001WO-US019444.  
XX  
XX 15-JUN-2000; 2000US-0212073P.  
XX  
XX 23-JUN-2000; 2000US-0213467P.  
XX  
XX 30-JUN-2000; 2000US-0215651P.  
XX  
XX 07-JUN-2000; 2000US-0216605P.  
XX  
XX 13-JUN-2000; 2000US-0218372P.  
XX  
XX 25-AUG-2000; 2000US-0228056P.  
XX  
XX (INCY-) INCYTE GENOMICS INC.

XX Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y;  
PI Gandhi AR, Tribouley CM, Wallia NK, Yao MG, Lu DAM, Greenwald SR;  
PI Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT;  
PI Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;  
PI Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L;  
PI Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;

XX WPI; 2002-090207/12.  
DR N-PSDB; AAD26472.  
XX  
PT New polypeptides, useful for diagnosing, treating or preventing disorders  
PT of growth and development, cardiovascular and lipid, and diseases such as  
PT cancer, comprise human kinase polypeptides.  
XX  
PS Claim 1; Page 173-174; 197pp; English.  
XX  
CC The invention relates to human kinase PKIN proteins and their  
CC corresponding cDNAs. A composition containing PKIN agonist is useful for  
CC treating a disease or condition associated with decreased expression of  
CC PKIN and a composition comprising PKIN antagonist is useful for treating  
CC a disease or condition associated with overexpression of PKIN. The  
CC disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma,  
CC myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder  
CC (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease,  
CC atherosclerosis, anaemia, allergies, adult respiratory distress syndrome,  
CC autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes  
CC mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease,  
CC osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,  
CC rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,  
CC bacterial, parasitic, fungal, viral, protozoal and helminthic infections)  
CC growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,  
CC Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio  
CC vascular disease (arteriovenous fistula, hypertension, vasculitis,  
CC aneurysms, congestive heart failure, angina pectoris, myocarditis,  
CC ischaemic heart disease, chronic bronchitis, lung tumours); lipid  
CC disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,  
CC hypcholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity  
CC of a test compound and in gene therapy. The present sequence is human  
CC PKIN-25 protein  
XX  
SQ Sequence 275 AA;

Query Match 57.2%; Score 1429; DB 5; Length 275;  
Best Local Similarity 100.0%; Pred. No. 4.2e-130;  
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 205 MVEDISELETAQKLEHNRNVRVPSYKILKVISADQPCVDVYQALTYVQSHRTN 264  
Db 1 MVEDISELETAQKLEHNRNVRVPSYKILKVISADQPCVDVYQALTYVQSHRTN 60  
QY 265 APPTPRVLLGPGVSGSKLQALLAQKYLNVNCCQLLKEAVADRTTGGELIQPFKE 324  
Db 61 APPTPRVLLGPGVSGSKLQALLAQKYLNVNCCQLLKEAVADRTTGGELIQPFKE 120  
QY 325 MAYPDSLLMKVLSQRLDQDCIQKQWLVHGVPRDLQAHLLNRLGYNPNRVFLNVPFDS 384  
Db 121 MAYPDSLLMKVLSQRLDQDCIQKQWLVHGVPRDLQAHLLNRLGYNPNRVFLNVPFDS 180  
QY 385 IMERLTLRRIDPVTGERVHLMKPPPTMEIQARLLNQLPKDAEQVKLKWDLFYNSADLE 444  
Db 181 IMERLTLRRIDPVTGERVHLMKPPPTMEIQARLLNQLPKDAEQVKLKWDLFYNSADLE 240  
QY 445 QLYGSALTILNGDQDPTVTFEYIESGIINPLPKIP 479  
Db 241 QLYGSALTILNGDQDPTVTFEYIESGIINPLPKIP 275

RESULT 8  
ADB65473  
ID ADB65473 standard; protein; 275 AA.  
XX  
XX ADB65473;  
XX  
DT 04-DEC-2003 (first entry)  
DE Human protein encoded by clone TEST120244460.  
XX Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;  
KW cell regeneration; membrane protein; signal transduction-related protein;



CC diseases involving haematopoietic stem cells (e.g., leukaemia), disorders  
CC involving B-cells (e.g., lymphoblastic leukaemia/lymphoma) and disorders  
CC involving precursor T-cell neoplasms. 27802 sequence is useful for  
CC modulating cellular growth and/or cellular metabolic pathways.  
CC particularly for regulating one or more proteins involved in growth and  
CC metabolism. 27802 DNA is used in gene therapy. 27802 sequence or its  
CC antibody are useful in screening assays, detection assays (e.g.,  
CC chromosomal mapping, tissue typing, forensic biology), preventive  
CC medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical  
CC trials and pharmacogenomics) and in methods of treatment  
XX  
SQ Sequence 258 AA;  
  
Query Match 52.0%; Score 1301; DB 4; Length 258;  
Best Local Similarity 99.6%; Pred. No. 1.1e-117;  
Matches 253; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 73 IAWWCKHLSLLTLENILNPFSTATARRLYLQKTVPSALLVQLIQERLAEDCI 132  
Db 1 MAWVCKHLSLLTLENILNPFSTATARRLYLQKTVPSALLVQLIQERLAEDCI 60  
  
Qy 133 KQWILGIPETREQALRIOTLGIPTPRHIVLSAPDVLIERNLGKRIDPQTGEIYHTTF 192  
Db 61 KQWILGIPETREQALRIOTLGIPTPRHIVLSAPDVLIERNLGKRIDPQTGEIYHTTF 120  
  
Qy 193 DWPESEIQNLRMVPEIDSELETAQKLLVYHRNIVRVPYKILKVISADQPCVDVFFQ 252  
Db 121 DWPESEIQNLRMVPEIDSELETAQKLLVYHRNIVRVPYKILKVISADQPCVDVFFQ 180  
  
Qy 253 ALTIVQSNHRTNAPFTPRVLLGPVSGKSLQALLAQAQYRLVNVCCGQLLKEAVADRTT 312  
Db 181 ALTIVQSNHRTNAPFTPRVLLGPVSGKSLQALLAQAQYRLVNVCCGQLLKEAVADRTT 240  
  
Qy 313 FGELIQPFPEKEMA 326  
Db 241 FGELIQPFPEKEMA 254  
  
RESULT 10  
ABW00581  
ID ABW00581 standard; protein; 258 AA.  
AC ABW00581;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human 27802, adenylate kinase protein.  
XX  
KW Human; ATPase-like protein; phosphatidylserine synthase-like protein;  
KW DNA fragmentation factor-like protein; vesicle-mediated transport;  
KW phospholipid scramblase-like protein; adenylate kinase protein;  
KW organelle biogenesis; cell-cycle regulation; primary brain lymphoma;  
KW protein degradation; splenomegaly; pulmonary embolism; Hodgkin disease;  
KW atresia; tuberculosis; astrocyte; apoptosis; neurodegenerative disease;  
KW DNA fragmentation; autoimmune disorder; cancer; blood clotting system;  
KW immune system; haematopoietic; hypertension; systemic sclerosis;  
KW atherosclerosis; leukaemia; oligodendrocyte; enzyme.  
XX  
OS Homo sapiens.  
XX  
FH Location/Qualifiers  
FT Modified-site 13 /note= "Asn is N-glycosylated"  
FT Modified-site 27..30  
FT Domain /note= "Casein kinase II (CK2) phosphorylation site"  
FT 41..120  
FT /note= "Domain 1"  
FT Modified-site 68..73  
FT /note= "N-myristoylation site"  
FT Modified-site 85..87  
FT /note= "Protein kinase C (PKC) phosphorylation site"  
FT Modified-site 93..96  
FT /note= "Casein kinase II (CK2) phosphorylation site"

FT Modified-site 104..107 /note= "Amidation site"  
FT Modified-site 118..121 /note= "Casein kinase II (CK2) phosphorylation site"  
FT Modified-site 139..142 /note= "Casein kinase II (CK2) phosphorylation site"  
FT Modified-site 196..198 /note= "Protein kinase C (PKC) phosphorylation site"  
FT Domain 201..251 /note= "Domain 1"  
FT Binding-site 203..210 /note= "ATP/GTP binding site motif"  
FT Modified-site 206..211 /note= "N-myristoylation site"  
FT Modified-site 207..209 /note= "Protein kinase C (PKC) phosphorylation site"  
FT Modified-site 240..243 /note= "Casein kinase II (CK2) phosphorylation site"

US2003092116-A1.

15-MAY-2003.

07-JUN-2002; 2002US-00165800.

10-FEB-2000; 2000US-0181705P.

29-FEB-2000; 2000US-0185609P.

29-FEB-2000; 2000US-0185946P.

29-FEB-2000; 2000US-0185947P.

29-FEB-2000; 2000US-0186234P.

12-FEB-2001; 2001US-00781677.

21-FEB-2001; 2001US-00790179.

21-FEB-2001; 2001US-00790180.

22-FEB-2001; 2001US-00790838.

26-FEB-2001; 2001US-00795038.

(MILL-) MILLENNIUM PHARM INC.

Chun M, Glucksmann MA, Kapeller-Libermann R, Meyers RE;

WPI; 2003-765479/72.

N-PSDB; AAD61170.

New isolated polypeptides including phosphatidylserine synthase-like polypeptide useful for identifying a compound which binds and modulates activity of the polypeptide useful for treating diseases, e.g. cancer.

Claim 8; Fig 28; Opp; English.

The present invention relates to novel proteins including ATPase-like proteins, phosphatidylserine synthase-like proteins, DNA fragmentation factor-like proteins, phospholipid scramblase-like proteins or adenylate kinase proteins and polynucleotides encoding such proteins. The human kinase-like molecules are useful for modulating ATPase function. They are useful in modulating organelle biogenesis, cell-cycle regulation, protein degradation and vesicle-mediated transport. They are also useful for treating disorders associated with aberrant ATPase-like expression or activity such as splenomegaly, pulmonary embolism, atresia and primary brain lymphoma. The human phosphatidylserine synthase-like molecules are useful for modulating the biosynthetic pathway involving the synthesis of the membrane phosphatidylserine (PS). They human phosphatidylserine synthase-like molecules are useful for treating disorders associated with aberrant human phosphatidylserine synthase activity such as tuberculosis, astrocytes and Hodgkin disease. The human 5698, DNA fragmentation factor-like molecules are useful for modulating apoptotic events, including DNA fragmentation. The human 5698 molecules are useful for treating diseases such as autoimmune disorders, neurodegenerative diseases and cancer. The human 32621, phospholipid scramblase-like molecules are useful for modulating immune, haematopoietic and blood clotting systems. They are useful for treating a disorder associated with aberrant human phospholipid scramblase-like protein activity such as leukaemia and systemic sclerosis. The human 27802 adenylate kinase are useful for modulating cellular growth and/or cellular metabolic pathways. They are

CC useful for treating hypertension, atherosclerosis and oligodendrocytes.  
 CC The present sequence is human 27802, adenylate kinase protein  
 XX  
 SQ Sequence 258 AA;

Query Match 52.0%; Score 1301; DB 7; Length 258;  
 Best Local Similarity 99.6%; Pred. No. 1.1e-117;  
 Matches 253; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 SQ  
 73 IAMWLKHLNSSLTLENIILNEFSYTATEARRLYLQKTVPSALLVQLIQLRLAEEDCI 132  
 :|||||  
 Db 1 MAMWLKHLNSSLTLENIILNEFSYTATEARRLYLQKTVPSALLVQLIQLRLAEEDCI 60  
 QY 133 KQWILGIPETREQALRIQTIGITPRHVIVLSAPDVTLLIERNLGRKIDPQTGEIYHTTF 192  
 :|||||  
 Db 61 KQWILGIPETREQALRIQTIGITPRHVIVLSAPDVTLLIERNLGRKIDPQTGEIYHTTF 120  
 QY 193 DWPESEIQNLMPEDISELETAQKLEHYNIRVIRVPSYKILKVISADQPCVDVIFYQ 252  
 :|||||  
 Db 121 DWPESEIQNLMPEDISELETAQKLEHYNIRVIRVPSYKILKVISADQPCVDVIFYQ 180  
 QY 253 ALTYVQSNHRTNAPFTRVLLGPGVSGKSLQAALLAQKYLNVNCCGQLLKEAVADRTT 312  
 :|||||  
 Db 181 ALTYVQSNHRTNAPFTRVLLGPGVSGKSLQAALLAQKYLNVNCCGQLLKEAVADRTT 240  
 QY 313 FGELIQPFPEKMA 326  
 :|||||  
 Db 241 FGELIQPFPEKMA 254

# RESULT 11

AAU40681  
 ID AAU40681 standard; protein; 240 AA.

AC AAU40681;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 5612.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia.

XX Homo sapiens.

OS WO200153312-A1.

PN 26-JUL-2001.

PP 26-DEC-2000; 2000WO-US034263.

PR 23-DEC-1999; 99US-00471275.

PR 21-JAN-2000; 2000US-00488725.

PR 25-APR-2000; 2000US-0052317.

PR 20-JUN-2000; 2000US-00598042.

PR 19-JUL-2000; 2000US-00620312.

PR 03-AUG-2000; 2000US-00653450.

PR 14-SEP-2000; 2000US-00662191.

PR 19-OCT-2000; 2000US-00693036.

PR 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang J, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
 PI Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.

DR N-PSDB; AA159837.

XX Novel nucleic acids and polypeptides, useful for treating disorders such  
 PT as central nervous system injuries.  
 XX

PS Example 2; SEQ ID NO 5612; 10078pp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and the  
 CC encoded polypeptides (AAM38642-AAM42213) with nootropic,  
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localized neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: immune system suppression,  
 CC activation/inhibition activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemias and  
 CC C.N.S disorders. Note: The sequence data for this patent did not form  
 CC part of the printed specification

XX Sequence 240 AA;

Query Match 47.4%; Score 1184.5; DB 4; Length 240;  
 Best Local Similarity 83.9%; Pred. No. 2.2e-106;  
 Matches 234; Conservative 0; Mismatches 0; Indels 45; Gaps 1;

QY 1 MDATIAPHRIPEMPQYGEENHIFELMQNMLEQLLIHQDEDPDIPFMIQHLHRDNDNVPRI 60  
 :|||||  
 Db 7 MDATIAPHRIPEMPQYGEENHIFELMQ----- 34

QY 61 VILGPPASGKTTIAMWLKHLNSSLTLENIILNEFSYTATEARRLYLQKTVPSALLVQ 120  
 :|||||  
 Db 35 -----AMWLKHLNSSLTLENIILNEFSYTATEARRLYLQKTVPSALLVQ 81

QY 121 LIQERLAEDCIKQWILGIPETREQALRIQTIGITPRHVIVLSAPDVTLLIERNLGRKI 180  
 :|||||  
 Db 82 LIQERLAEDCIKQWILGIPETREQALRIQTIGITPRHVIVLSAPDVTLLIERNLGRKI 141

QY 181 DPQTGETYHTTDPWPESEIQNLMPEDISELETAQKLEHYNIRVIRVPSYKILKVI 240  
 :|||||  
 Db 142 DPQTGETYHTTDPWPESEIQNLMPEDISELETAQKLEHYNIRVIRVPSYKILKVI 201

QY 241 SAQPCVDVIFYQALTYVQSNHRTNAPFTRVLLGPGVGS 279  
 :|||||  
 Db 202 SAQPCVDVIFYQALTYVQSNHRTNAPFTRVLLGPGVGS 240

## RESULT 12

AAU17305

ID AAU17305 standard; protein; 236 AA.

AC AAU17305;

DT 07-NOV-2001 (first entry)

DE Novel signal transduction pathway protein, Seq ID 870.

XX Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;  
 KW antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;  
 KW immune system disorder; rheumatoid arthritis; inflammatory condition;  
 KW organ transplant rejection; infection; hepatitis C; blood disorder;  
 KW sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;  
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;  
 KW chromosomal abnormality; Down syndrome; ischaemia; renal disorder;  
 KW cardiovascular; respiratory; wound healing; endocrine; Addison's disease;  
 KW reproductive system; gastrointestinal; liver disorder; AIDS;  
 KW acquired immune deficiency syndrome.

OS Homo sapiens.

XX WO200154733-A1.

XX	PR	29-SEP-2000;	2000US-0236367P.
XX	PR	29-SEP-2000;	2000US-0236368P.
PD	PR	29-SEP-2000;	2000US-0236369P.
XX	PR	29-SEP-2000;	2000US-0236370P.
PF	PR	02-OCT-2000;	2000US-0236802P.
XX	PR	02-OCT-2000;	2000US-0237037P.
XX	PR	02-OCT-2000;	2000US-0237038P.
PR	PR	02-OCT-2000;	2000US-0237039P.
PR	PR	02-OCT-2000;	2000US-0237040P.
PR	PR	13-OCT-2000;	2000US-0239935P.
PR	PR	13-OCT-2000;	2000US-0239937P.
PR	PR	20-OCT-2000;	2000US-0240960P.
PR	PR	20-OCT-2000;	2000US-0241221P.
PR	PR	20-OCT-2000;	2000US-0241785P.
PR	PR	20-OCT-2000;	2000US-0241786P.
PR	PR	20-OCT-2000;	2000US-0241787P.
PR	PR	20-OCT-2000;	2000US-0241808P.
PR	PR	20-OCT-2000;	2000US-0241809P.
PR	PR	20-OCT-2000;	2000US-0241825P.
PR	PR	01-NOV-2000;	2000US-0244617P.
PR	PR	08-NOV-2000;	2000US-0246474P.
PR	PR	08-NOV-2000;	2000US-0246475P.
PR	PR	08-NOV-2000;	2000US-0246476P.
PR	PR	08-NOV-2000;	2000US-0246477P.
PR	PR	08-NOV-2000;	2000US-0246478P.
PR	PR	08-NOV-2000;	2000US-0246523P.
PR	PR	08-NOV-2000;	2000US-0246524P.
PR	PR	08-NOV-2000;	2000US-0246525P.
PR	PR	08-NOV-2000;	2000US-0246526P.
PR	PR	08-NOV-2000;	2000US-0246527P.
PR	PR	08-NOV-2000;	2000US-0246528P.
PR	PR	08-NOV-2000;	2000US-0246532P.
PR	PR	08-NOV-2000;	2000US-0246609P.
PR	PR	08-NOV-2000;	2000US-0246610P.
PR	PR	08-NOV-2000;	2000US-0246611P.
PR	PR	08-NOV-2000;	2000US-0246613P.
PR	PR	17-NOV-2000;	2000US-0248207P.
PR	PR	17-NOV-2000;	2000US-0249208P.
PR	PR	17-NOV-2000;	2000US-0249209P.
PR	PR	17-NOV-2000;	2000US-0249210P.
PR	PR	17-NOV-2000;	2000US-0249211P.
PR	PR	17-NOV-2000;	2000US-0249212P.
PR	PR	17-NOV-2000;	2000US-0249213P.
PR	PR	17-NOV-2000;	2000US-0249214P.
PR	PR	17-NOV-2000;	2000US-0249215P.
PR	PR	17-NOV-2000;	2000US-0249216P.
PR	PR	17-NOV-2000;	2000US-0249217P.
PR	PR	17-NOV-2000;	2000US-0249218P.
PR	PR	17-NOV-2000;	2000US-0249244P.
PR	PR	17-NOV-2000;	2000US-0249245P.
PR	PR	17-NOV-2000;	2000US-0249264P.
PR	PR	17-NOV-2000;	2000US-0249265P.
PR	PR	17-NOV-2000;	2000US-0249297P.
PR	PR	17-NOV-2000;	2000US-0249299P.
PR	PR	17-NOV-2000;	2000US-0249300P.
PR	PR	01-DEC-2000;	2000US-0250160P.
PR	PR	01-DEC-2000;	2000US-0250391P.
PR	PR	05-DEC-2000;	2000US-0251030P.
PR	PR	05-DEC-2000;	2000US-0251988P.
PR	PR	05-DEC-2000;	2000US-0255719P.
PR	PR	06-DEC-2000;	2000US-0251479P.
PR	PR	08-DEC-2000;	2000US-0251856P.
PR	PR	08-DEC-2000;	2000US-0251868P.
PR	PR	08-DEC-2000;	2000US-0251869P.
PR	PR	08-DEC-2000;	2000US-0251989P.
PR	PR	08-DEC-2000;	2000US-0251990P.
PR	PR	11-DEC-2000;	2000US-0254097P.
PR	PR	03-JAN-2001;	2001US-02554097P.
XX	XX		
XX	PA	(HUMA-) HUMAN GENOME SCI INC.	
XX	XX		
XX	PI	Rosen CA, Barash SC, Ruben SM;	
XX	XX		

DR WPI: 2001-465460/50.  
 DR N-PSDB; AAS27222.  
 XX Novel polypeptides useful for diagnosing, treating, preventing and/or.  
 PT prognosing disorders related to the proteins, including cancers, immune  
 PT disorders and neuronal disorders.  
 XX  
 PS Claim 1; SEQ ID NO 870; 880pp; English.  
 XX  
 CC The invention relates to novel isolated polypeptides (I), and  
 CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for  
 CC diagnosing, preventing and treating diseases including immune system  
 CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune  
 CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ  
 CC transplant rejections and graft versus host disease, infectious diseases  
 CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and  
 CC other blood-related disorders (sickle cell anaemia), myeloproliferative  
 CC disorders, primary haematopoietic disorders, hyperproliferative disorders  
 CC (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.  
 CC Alzheimer's disease, Parkinson's disease), chromosomal abnormalities  
 CC (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.  
 CC glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),  
 CC respiratory disorders, dermatological disorders, in wound healing,  
 CC epithelial cell proliferation, endocrine disorders (e.g. Addison's  
 CC disease), reproductive system disorders, gastrointestinal disorder  
 CC (inflammatory disorders), liver disorders (cirrhosis), as stimulators of  
 CC B-cell responsiveness to pathogens, activators of T-cells, to induce  
 CC higher affinity antibodies, and as a means to induce tumour proliferation  
 CC in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-  
 CC AAU17683 represent novel signal transduction pathway protein, amino acid  
 CC sequences of the invention  
 XX

Query Match 46.6%; Score 1166; DB 4; Length 236;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-104;  
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 147 QALRIQTLGTPRHVILSAPDTVLIERNLGKIDPQTGRIYHTTFDWPPESEIONRLMV 206  
 DB 1 QALRIQTLGTPRHVILSAPDTVLIERNLGKIDPQTGRIYHTTFDWPPESEIONRLMV 60  
 OY 207 PEDISETLAQKLEVHRNIVRIPSYKILKVISADQPCVYQALTYVQSNRTNAP 266  
 DB 61 PEDISETLAQKLEVHRNIVRIPSYKILKVISADQPCVYQALTYVQSNRTNAP 120  
 OY 267 FTRVLLGLGVGSGKSLQALLAQLRYLVNVCQQLKEAVADRTTFGLIOPPFKEKMA 326  
 DB 121 FTRVLLGLGVGSGKSLQALLAQLRYLVNVCQQLKEAVADRTTFGLIOPPFKEKMA 180  
 OY 327 VPDSLLMKVLSQRLDQDCIQKGWLVHGVPRDLDDQHLNRLGYN 371  
 DB 181 VPDSLLMKVLSQRLDQDCIQKGWLVHGVPRDLDDQHLNRLGYN 225

RESULT 13  
 ADB94013  
 ID ADB94013 standard; protein; 236 AA.  
 AC ADB94013;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Human novel protein #247.  
 XX  
 KW human; autoimmune disease; Parkinson's disease; silicosis;  
 KW gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia;  
 KW immunosuppressive agent; adjuvant; enhance immune response;  
 KW higher affinity antibody induction;  
 KW increased serum immunoglobulin concentration.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002169711-A1.

XX  
 PD 14-NOV-2002.  
 XX  
 PF 17-JAN-2001; 2001US-00764868.  
 XX  
 PR 31-JAN-2000; 2000US-0179065P.  
 PR 04-FEB-2000; 2000US-0180628P.  
 PR 28-JUN-2000; 2000US-0214886P.  
 PR 07-JUL-2000; 2000US-0216847P.  
 PR 07-JUL-2000; 2000US-0216880P.  
 PR 11-JUL-2000; 2000US-0217487P.  
 PR 14-JUL-2000; 2000US-0218290P.  
 PR 26-JUL-2000; 2000US-0220963P.  
 PR 14-AUG-2000; 2000US-0220964P.  
 PR 14-AUG-2000; 2000US-0224518P.  
 PR 14-AUG-2000; 2000US-0225267P.  
 PR 14-AUG-2000; 2000US-0225268P.  
 PR 14-AUG-2000; 2000US-0225270P.  
 PR 14-AUG-2000; 2000US-0225447P.  
 PR 14-AUG-2000; 2000US-0225757P.  
 PR 22-AUG-2000; 2000US-0225758P.  
 PR 20-AUG-2000; 2000US-0226868P.  
 PR 01-SEP-2000; 2000US-0228924P.  
 PR 01-SEP-2000; 2000US-0229287P.  
 PR 01-SEP-2000; 2000US-0229343P.  
 PR 01-SEP-2000; 2000US-0229344P.  
 PR 05-SEP-2000; 2000US-0229345P.  
 PR 05-SEP-2000; 2000US-0229509P.  
 PR 08-SEP-2000; 2000US-0229513P.  
 PR 21-SEP-2000; 2000US-0231413P.  
 PR 21-SEP-2000; 2000US-0234223P.  
 PR 25-SEP-2000; 2000US-0234224P.  
 PR 27-SEP-2000; 2000US-0234597P.  
 PR 29-SEP-2000; 2000US-0235834P.  
 PR 29-SEP-2000; 2000US-0236327P.  
 PR 29-SEP-2000; 2000US-0236367P.  
 PR 29-SEP-2000; 2000US-0236368P.  
 PR 29-SEP-2000; 2000US-0236369P.  
 PR 02-OCT-2000; 2000US-0236370P.  
 PR 02-OCT-2000; 2000US-0236802P.  
 PR 02-OCT-2000; 2000US-0237037P.  
 PR 02-OCT-2000; 2000US-0237038P.  
 PR 02-OCT-2000; 2000US-0237039P.  
 PR 13-OCT-2000; 2000US-0237040P.  
 PR 20-OCT-2000; 2000US-0240960P.  
 PR 20-OCT-2000; 2000US-0241785P.  
 PR 20-OCT-2000; 2000US-0241809P.  
 PR 01-NOV-2000; 2000US-0244617P.  
 PR 17-NOV-2000; 2000US-0249299P.  
 PR 08-DEC-2000; 2000US-0251856P.  
 PR 08-DEC-2000; 2000US-0251868P.  
 PR 08-DEC-2000; 2000US-0251869P.  
 XX  
 PA (ROSE/) ROSEN C A.  
 PA (RUBE/) RUBEN S M.  
 PA (BARA/) BARASH S C.  
 XX  
 PI Rosen CA, Ruben SM, Barash SC;  
 XX  
 DR WPI; 2003-719985/68.  
 DR N-PSDB; ADB93390.  
 XX  
 PT New isolated polypeptide useful for diagnosing and treating  
 PT immunosuppressive conditions such as autoimmune disease and Parkinson's  
 PT disease.  
 XX  
 PS Claim 11; SEQ ID NO 870; 345pp; English.  
 XX  
 CC The invention relates to an isolated polypeptide. The polypeptide is  
 CC useful for diagnosing a pathological condition or a susceptibility to a





PN WO200157190-A2.  
XX  
PD 09-AUG-2001.  
XX  
XX 05-FEB-2001; 2001WO-US004098.  
XX  
XX 03-FEB-2000; 2000US-00496914.  
PR 27-APR-2000; 2000US-00560875.  
PR 20-JUN-2000; 2000US-00598075.  
PR 19-JUL-2000; 2000US-00620325.  
PR 01-SEP-2000; 2000US-00654936.  
PR 15-SEP-2000; 2000US-00663561.  
PR 20-OCT-2000; 2000US-00693325.  
PR 30-NOV-2000; 2000US-00728422.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;  
PI Ma Y, Zhao QN, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;  
PI Xue AJ, Yang Y, Wejhrman I, Goodrich R;  
XX WPI; 2001-476283/51.  
DR N-PSDB; AAK52534.  
XX  
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful  
PT in diagnosis and gene therapy.  
XX  
XX Claim 20; Page 237; 6221pp; English.  
XX  
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the  
CC encoded polypeptides (AAW78123-AAW80102) that exhibit activity elating to  
CC cytokine cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, haematopoiesis regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activin/inhibin activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111  
CC (AAK52582) and 3666 (AAW80020) are omitted as the relevant pages from the  
CC sequence listing were missing at the time of publication  
XX  
XX Sequence 226 AA;  
SQ  
Query Match 32.0%; Score 800; DB 4; Length 226;  
Best Local Similarity 99.3%; Pred. No. 5.5e-69;  
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 327 VPSLLMKVLSQLDQDCIQKGVHLGVPRDLDOAHLNRLGYNPNRVFFLNVPFDSIM 386  
Db 74 VPSLLMKVLSQLDQDCIQKGVHLGVPRDLDOAHLNRLGYNPNRVFFLNVPFDSIM 133  
QY 387 ERLTLRRIDPVTGERVHLMYKPPPTWEIQARLLQNPKDAEQVKLKMDFYRNSADLEQL 446  
Db 134 ERLTLRRIDPVTGERVHLMYKPPPTWEIQARLLQNPKDAEQVKLKMDFYRNSADLEQL 193  
QY 447 YGSATLNGDQDPVTVPVEIESGIINPLPKIP 479  
Db 194 YGSATLNGDQDPVTVPVEIESGIINPLPKIP 226  
Search completed: March 18, 2005, 15:17:38  
Job time : 173 secs

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	Query Match	10.9%; Score 273; DB 2; Length 212;
	Best Local Similarity	31.6%; Pred. No. 1.2e-11;
	Matches	67; Conservative 46; Mismatches 85; Indels 14; Gaps 4;
QY	271 VLLGPGVGSKLQAALLAQKYLNVNCCQLLKAEVAORTTFGGELIQDFFEKEMAVPDS	330
DB	3 LLMLGLPGAGKGTAQAAIKVEQHFAHISTGDMPRAAMANTMGVLAKSYIDKGEIYPDE	62
QY	331 LLMKVLSRLDDQCCTQKGVNLHGVRDLDOAHILNR---	LGYNENRVPFLNVDPDSIM 386
DB	63 VTNGIVKERLSODDIKETGFLLDGYPRTIEQAALDKTTLAELGIIEGVINIEVNPDSL	122
QY	387 ERIITLARIPDVTCERVHLMYKPPTMEIOARLLQNPKDAEEQVKLRMDLPFRNSADLEQL	446
DB	123 ERUSGRILIHVTGETFHKVFNPVDYK-BEDYYQRDDKPETVKRRLDV---NTAQOGEPI	178
QY	447 Y-----GSAILTGQQDPVTVFEYTEISGIN 472	
DB	179 IAHVRAGKLGHVDIEGNQINDVFSDEIKULTN 210	
<b>RESULT 4</b>		
B97898	adenylate kinase (EC 2.7.4.3) [imported] - Streptococcus pneumoniae (strain R6)	
C:	Species:	Streptococcus pneumoniae
C:	Date:	22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:	Accession:	B97898
E:	R.; Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoffhoff, P.; McAhr,	
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McArthur,		
J. Bacteriol.	183; 5709-5717, 2001	
A:	Authors:	Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskur
A:	Title:	Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:	Reference number:	A97872; PMID:11544234
A:	Accession:	B97898
A:	Status:	Preliminary
A:	Molecule type:	DNA
A:	Residues:	1-212 <KUR>
A:	Cross-references:	UNIPROT:Q8DRD4; GB:AE007317; PIDN:AAK99014.1; PID:g1545775S
C:	Genetics:	
A:	Gene:	adk
C:	Superfamily:	adenylate kinase
C:	Keywords:	phosphotransferase
<b>Query Match</b>		
	Best Local Similarity	10.9%; Score 272; DB 2; Length 212;
	Matches	66; Conservative 47; Mismatches 85; Indels 14; Gaps 4;

[illegible]

A>Title: Sequence analysis of a 32-kb region including the major ribosomal protein gene  
A/Reference number: 222756; MUID:99209008; PMID:10192928  
A/Accession: Y44404  
A>Status: preliminary; translated from GB/EMBL/DBEY  
A/Molecule type: DNA  
A/Residues: 1-217 <TAK>  
A/Cross-references: UNIPROT:P38372; EMBL:AB017508; NID:94512395; PIDN:BA075292.1; PID:94  
A/Experimental source: strain C-125  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira  
Nucleic Acids Res. 28, 4317-4331, 2000  
A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A/Reference number: A83650; MUID:20512582; PMID:11058132  
A/Accession: C83669  
A>Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-217 <STO>  
A/Cross-references: GB:AP001507; GB:BA000004; NID:G10172612; PIDN:BA03874.1; GSPDB:GN00  
A/Experimental source: strain C-125  
C/Genetics:  
A/Genes: adk  
C/Superfamily: adenylate kinase  
C/Keywords: phosphotransferase

Query Match 10.9%; Score 272; DB 2; Length 217;  
Best Local Similarity 31.3%; Pred. No. 1.4e-11;  
Matches 66; Conservative 42; Mismatches 83; Indels 20; Gaps 5;

QY 271 VLLGPGVSGSLQAALLAOKYRLVNVCCGQLLKAVADRTTFGELIQPFKEKMAVPDS 330  
DB 3 LILMGLPGAGGTQAEIKIIEYGIPIHSTGDMFRAAMKNETELGLKAKSYMDAGELVPDE 62

QY 331 LMKVLSORLQDQDCIOKQWLVHGVPRDLQAHLLNRLGYNPNRPFDS 389  
DB 63 VTIGVDRLSQDDC-QNGFLDGFPRTPVAQAEALDILASLDKLDY---VINIDVPE 117

QY 383 DSIMERLTRIDPVTGERHYLMYKPPPTMEI---QARLLQNPKDAEQVKLMDL 389  
DB 118 QLLMDRLTGRRVSPSTGRTHVFNPPKVEGICVDVSGSELIQRDDDKPFTVKRLVFNQK 177

QY 439 NSADLEQLY---GSAITLNGDDPVTVEYI 466  
DB 178 QAQPLDFYSEKGYLQNINGDDQISRKFEDI 208

RESULT 6  
H97282  
adenylate kinase [imported] - Clostridium acetobutylicum  
C/Species: Clostridium acetobutylicum  
C/Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C/Accession: H97282  
R:Nolling, J.; Breton, G.; Omselchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl  
A/Reference number: A96900; MUID:21359325; PMID:21359325  
A/Accession: H97282  
A>Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-215 <KUR>  
A/Cross-references: UNIPROT:Q97E99; GB:AE001437; PIDN:AAK81051.1; PID:G15026178; GSPDB:G  
A/Experimental source: Clostridium acetobutylicum ATCC824  
C/Genetics:  
A/Genes: CAC3112  
C/Superfamily: adenylate kinase

Query Match 10.4%; Score 260; DB 2; Length 215;  
Best Local Similarity 27.6%; Pred. No. 9.5e-11;  
Matches 60; Conservative 52; Mismatches 79; Indels 26; Gaps 5;

QY 270 RVLLGPGVSGSLQAALLAOKYRLVNVCCGQLLKAVADRTTFGELIQPFKEKMAVPD 329  
DB 2 KIILLGPGAGGTQAKIISSEFSIPHISTGDIIFRANISGKTELGMKAKGYMDKGLVLPD 61

A>Title: Sequence analysis of a 32-kb region including the major ribosomal protein gene  
A/Reference number: 222756; MUID:99209008; PMID:10192928  
A/Accession: Y44404  
A>Status: preliminary; translated from GB/EMBL/DBEY  
A/Molecule type: DNA  
A/Residues: 1-217 <TAK>  
A/Cross-references: UNIPROT:P38372; EMBL:AB017508; NID:94512395; PIDN:BA075292.1; PID:94  
A/Experimental source: strain C-125  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira  
Nucleic Acids Res. 28, 4317-4331, 2000  
A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A/Reference number: A83650; MUID:20512582; PMID:11058132  
A/Accession: C83669  
A>Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-217 <STO>  
A/Cross-references: GB:AP001507; GB:BA000004; NID:G10172612; PIDN:BA03874.1; GSPDB:GN00  
A/Experimental source: strain C-125  
C/Genetics:  
A/Genes: adk  
C/Superfamily: adenylate kinase  
C/Keywords: phosphotransferase

Query Match 10.3%; Score 257.5; DB 2; Length 214;  
Best Local Similarity 29.6%; Pred. No. 1.4e-10;  
Matches 55; Conservative 47; Mismatches 73; Indels 11; Gaps 3;

QY 270 RVLLGPGVSGSLQAALLAOKYRLVNVCCGQLLKAVADRTTFGELIQPFKEKMAVPD 329  
DB 2 RIILLGPGAGGTQAEIKIIEYGIPIHSTGDMFRAAMKNETELGLKAKSYMDAGELVPDE 61

QY 330 LMKVLSORLQDQDCIOKQWLVHGVPRDLQAHLLNRLGYNPNRPFDS 389  
DB 62 DIILLGPKERIAQADC-EKGLDGFPRTPVAQAEALDILASLDKLDY---VINIDVPE 117

QY 390 TLRIDPVTGERHYLMYKPPPTMEIQAAR-----LLQNPKDAEQVKLMDL 389  
DB 121 AGSRALPSPGRTYHVYVNPFP---KVEGKDDVTGDELIVREDDKSTVRLVRLVHTQTAP 177

QY 443 LEQLYG 448  
DB 178 LIEYTG 183

RESULT 8  
S43016  
adenylate kinase (EC 2.7.4.3) - Bordetella pertussis  
N/Alternate names: ATP-AMP transphosphorylase  
C/Species: Bordetella pertussis  
C/Date: 07-Sep-1994 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C/Accession: S43016  
R:Gilles, A.M.; Sismeiro, O.; Munier, H.; Fabian, H.; Mantsch, H.H.; Surewicz, W.K.; Cra  
Eur. J. Biochem. 218, 921-927, 1993  
A>Title: Structural and physico-chemical characteristics of Bordetella pertussis adenyly  
A/Reference number: S43016; MUID:94109391; PMID:8281944  
A/Accession: S43016  
A/Molecule type: DNA  
A/Residues: 1-218 <GIL>  
A/Cross-references: UNIPROT:P39069; EMBL:Z29715; NID:G453620; PIDN:CAA82801.1; PID:G4536  
A/Experimental source: strain 18323

C;Genetics: 10.38; Score 255.5; DB 2; Length 218;  
A;Gene: adk  
C;Function: Best Local Similarity 32.18; Pred. No. 1.7e-10;  
A;Description: catalyzes reversible phosphorylation of AMP with ATP to form two ADP  
Matches 59; Conservative 34; Mismatches 86; Indels 5; Gaps 2;  
C;Superfamily: adenylyate kinase  
C;Keywords: ATP; P-loop; phosphotransferase  
F;7-14/Region: nucleotide-binding motif A (P-loop) #status atypical  
F;80-85/Region: nucleotide-binding motif B #status atypical  
F;30,84,126/Active site: Ser, Asp, His #status predicted

QY 270 RVLILGPGVSGKSLQAALLAQKYLKLVNVCQQLKEAVADRTTFGELIQFFKEMAVPD 329  
DB 2 RLILGPGAGKGTQAAFLTQHYGIPQISTGDMRLAAVKAAGTGLGLEAKKVMWDAGGLVSD 61

QY 330 SLMLKVLSQLDQDCIQKGVHLGVPRDLDOAHLNRLGVNPNRVFFLNVPFDSIMERL 389  
DB 62 DLIIGLVDRDLTPDC-ANGYLPDFGFPRTIPQADALSKAGIALDYVVEIVPSPDIIERM 120

QY 390 TLRRIDPVTGXYHLMVKKPPTMEIQ-----ARLLQNPKEAEQVKLMDLFYRNSADLEQ 445  
DB 121 SERRVHPASGRSYHVRNPPKAEQVDVTGELVQRDDRETVRHLNLYVQNTPLVD 180

QY 446 LYGS 449  
DB 181 YVSS 184

RESULT 9  
G70307  
adenylate kinase (EC 2.7.4.3) - Aquifex aeolicus  
C;Species: Aquifex aeolicus  
C;Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
C;Accession: G70307  
R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.

Nature 392, 353-358, 1998  
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A;Reference number: A70300; MUID:98196666; PMID:9537320  
A;Accession: G70307  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-206 <AQF>  
A;Cross-references: UNIPROT:O66490; GB:AE000672; NID:92982810; PIDN:AAC06438.1; PID:g298  
A;Experimental source: strain VF5  
C;Genetics:  
A;Gene: kad  
C;Function: catalyzes reversible phosphorylation of AMP with ATP to form two ADP  
A;Note: magnesium required  
C;Superfamily: adenylyate kinase  
C;Keywords: ATP; P-loop; phosphotransferase  
F;7-14/Region: nucleotide-binding motif A (P-loop) #status atypical  
F;77-82/Region: nucleotide-binding motif B #status atypical  
F;28,81/Active site: His, Asp #status predicted

Query Match 10.28; Score 255.5; DB 2; Length 206;  
Best Local Similarity 30.94; Pred. No. 1.8e-10;  
Matches 56; Conservative 42; Mismatches 72; Indels 11; Gaps 3;

QY 271 VLLILGPGVSGKSLQAALLAQKYLKLVNVCQQLKEAVADRTTFGELIQFFKEMAVPD 330  
DB 3 LVFLGPGAGKGTQAAFLTQHYGIPQISTGDMRLAAVKAAGTGLGLEAKKVMWDAGGLVSD 62

QY 331 LLMKVLSQLDQDCIQKGVHLGVPRDLDOA-----HLNRLGVNPNRVFFLNVPFDSIM 386  
DB 63 LIILALIEVFPKGNV-----IFDGFPRTVQKAEALDEMLEKGLKGVHLLFVDPVVI 118

QY 387 ERLTLRIDPVTGXYHLMVKKPPTMEIQARLLQNPKEAEQVKLMDLFYRNSADLEQ 446

DB 119 ERLSGRINPTEGVYHVKYNPPPP---GVKVIQREDDKPEVKKRLEVREQTAPLIEY 175  
QY 447 Y 447  
DB 176 Y 176

RESULT 10  
J50492  
adenylate kinase (EC 2.7.4.3) - Bacillus subtilis  
A;Alternate names: ATP-AMP transphosphorylase  
C;Species: Bacillus subtilis  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C;Accession: J50492; S12684; S08630; B69583  
R;Nakamura, K.; Nakamura, A.; Takamatsu, H.; Yoshikawa, H.; Yamane, K.  
J. Biochem. 107, 603-607, 1990  
A;Title: Cloning and characterization of a Bacillus subtilis gene homologous to E. coli  
A;Reference number: J50490; MUID:90292990; PMID:2113521  
A;Accession: J50492  
A;Molecule type: DNA  
A;Residues: 1-217 <NAK>  
A;Cross-references: UNIPROT:P16304; GB:D00619; NID:g216336; PIDN:BAA00496.1; PID:g216340  
R;Yoshikawa, H.; Doi, R.H.  
Nucleic Acids Res. 18, 1647, 1990  
A;Title: Sequence of the Bacillus subtilis spectinomycin resistance gene region.  
A;Reference number: S12680; MUID:90221911; PMID:2139212  
A;Accession: S12684  
A;Molecule type: DNA  
A;Residues: 1-116 <YOS>  
A;Cross-references: EMBL:M31102; NID:g1184272; PIDN:AAB59119.1; PID:g143579  
R;Experimental source: strain 1A241  
R;Suh, J.W.; Boylan, S.A.; Thomas, S.M.; Dolan, K.M.; Oliver, D.B.; Price, C.W.  
Mol. Microbiol. 4, 305-314, 1990  
A;Title: Isolation of a secY homologue from Bacillus subtilis: evidence for a common pro.  
A;Reference number: S08628; MUID:90251170; PMID:2110998  
A;Accession: S08630  
A;Molecule type: DNA  
A;Residues: 1-99 <SUH>  
A;Cross-references: EMBL:X51329; NID:g40132; PIDN:CAA35713.1; PID:g40135  
R;Experimental source: strain Marburg; cell line PB2  
R;Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter  
C.; Bron, S.; Brouillet, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho  
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabre, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler  
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maguda, S.; Mausel,  
Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,  
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winter, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.  
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A;Reference number: A69580; MUID:98044033; PMID:9384377  
A;Accession: B69583  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-217 <KUN>  
A;Cross-references: GB:Z99104; GB:AL009126; NID:g2632267; PIDN:CAB11913.1; PID:g2632404  
R;Experimental source: strain 168  
C;Genetics:  
A;Gene: adk  
C;Function: catalyzes reversible phosphorylation of AMP with ATP to form two ADP  
A;Note: magnesium required  
C;Superfamily: adenylyate kinase  
C;Keywords: ATP; P-loop; phosphotransferase  
F;7-14/Region: nucleotide-binding motif A (P-loop) #status atypical  
F;80-85/Region: nucleotide-binding motif B #status atypical  
F;28,84/Active site: His, Asp #status predicted



Query Match 10.0%; Score 249; DB 2; Length 217;  
Best Local Similarity 30.4%; Pred. No. 5.5e-10;  
Matches 62; Conservative 41; Mismatches 89; Indels 12; Gaps 4;  
QY 271 VLLGPGVSGSLQALLAOKYRLVNVCCGOLLKEAVADRTTFGELIQPFPEKEMAVPDS 330  
D 3 LVLMLGPGAGGTQGERIVEDYGPISITGDMFRAKKEETPLGLEAKSYIDGELVPDE 62  
QY 331 LLMKVLSQLDQDCIOKGVNLGVPRDLQAHLLNRLGYNPNRVFFLNVPFDSIM 386  
D 63 VTGIVKRLKDDC-ERGLDGFPTTQAEALAEILEYKRPIDYVINIEVDKVL 121  
QY 387 ERLTLRRIDPVTGERHYLMYKPPPTMEI---QARLLQNPDAEQVKMLKMDLFYRNSAD 442  
D 122 ERLTLRRICSCGTTTHLVFNPPKPTFGICDKGGELYQRADNNEETVSKRLVNMKQTP 181  
QY 443 LEQLY---GSAITLNGDQDPYTF 463  
D 182 LLDYSEKGYLANVNGQDIQDY 205

## RESULT 11

H90019  
adenylate kinase [imported] - Staphylococcus aureus (strain N315)  
C:Species: Staphylococcus aureus  
C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: H90019  
R:Auroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
Lancet 357, 1225-1240, 2001  
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.  
A:Reference number: A89758; PMID:21311952; PMID:11418146  
A:Accession: H90019  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-215 <KUR>  
A:Cross-references: UNIPROT:Q9S40; GB:BA000018; PID:g13702029; PIDN:BA843321.1; GSPDB:G  
A:Experimental source: strain N315  
A:Genetics:  
A:Gene: adk  
C:Superfamily: adenylate kinase

Query Match 9.7%; Score 242; DB 2; Length 215;  
Best Local Similarity 28.1%; Pred. No. 1.6e-09;  
Matches 56; Conservative 48; Mismatches 83; Indels 12; Gaps 4;  
QY 271 VLLGPGVSGSLQALLAOKYRLVNVCCGOLLKEAVADRTTFGELIQPFPEKEMAVPDS 330  
D 3 ILLMLGPGAGGTQASEIVKKEPPIPHISTGDMFRAKKEETPLGLEAKSYIDGELVPDE 62  
QY 331 LLMKVLSQLDQDCIOKGVNLGVPRDLQAHLLNRLGYNPNRVFFLNVPFDSIM 386  
D 63 VTGIVKRLKDDC-ERGLDGFPTTQAEALAEILEYKRPIDYVINIEVDKVL 121  
QY 387 ERLTLRRIDPVTGERHYLMYKPPPTMEI---QARLLQNPDAEQVKMLKMDLFYRNSAD 442  
D 122 NRLTLRRICSCGTTTHLVFNPPKPTFGICDKGGELYQRADNNEETVSKRLVNMKQTP 181  
QY 443 LEQLY---GSAITLNGDQ 458  
D 182 ILDFYDQKGVNLKIDGSKD 200

## RESULT 12

B84986  
adenylate kinase (EC 2.7.4.3) [imported] - Buchnera sp. (strain APS)  
C:Species: Buchnera sp.  
C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001  
C:Accession: B84986  
R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.  
Nature 407, 81-86, 2000

A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. ?  
A:Reference number: A84930; PMID:2045173; PMID:10993077  
A:Accession: B84986  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-215 <STO>  
A:Cross-references: GB:AP000398; GSPDB:GN00144  
A:Experimental source: strain APS  
C:Genetics:  
A:Gene: adk; BU484  
C:Superfamily: adenylate kinase  
C:Keywords: phosphotransferase

Query Match 9.7%; Score 241.5; DB 2; Length 215;  
Best Local Similarity 28.6%; Pred. No. 1.8e-09;  
Matches 52; Conservative 44; Mismatches 81; Indels 5; Gaps 2;  
QY 270 RVLLGPGVSGSLQALLAOKYRLVNVCCGOLLKEAVADRTTFGELIQPFPEKEMAVPD 329  
D 2 RIILLGAPGTGKTQCKFITEKYKIPQISTGDMLESVVLKNGIKMINKIIEEGKLYSD 61  
QY 330 SLLMKVLSQRLDQDCIOKGVNLGVPRDLQAHLLNRLGYNPNRVFFLNVPFDSIMERL 389  
D 62 EIVCHLIKRNKIKKDCI-NGFLDGFPTTQALYLSKKNIKIDYVLEFIIPHEYLRI 120  
QY 390 TLRRIDPVTGERHYLMYKPPPTMEI---IQARLLQNPDAEQVKMLKMDLFYRNSADLEQ 445  
D 121 SGRIHQSGRIYHVKFPKPKDKDDLTCGTLTKRDKDKGKRLKEKVKVHDPLVQ 180  
QY 446 LY 447  
D 181 YY 182

## RESULT 13

AG0378  
adenylate kinase (EC 2.7.4.3) [imported] - Yersinia pestis (strain CO92)  
C:Species: Yersinia pestis  
C>Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
C:Accession: AG0378  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.M.; Davis, P.; Dougan, G.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; PMID:21470413; PMID:11586360  
A:Accession: AG0378  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-214 <KUR>  
A:Cross-references: UNIPROT:O69172; GB:AL590842; PIDN:CAC92354.1; PID:g15981059; GSPDB:G  
A:Genetics:  
A:Gene: adk  
C:Superfamily: adenylate kinase  
C:Keywords: phosphotransferase

Query Match 9.6%; Score 240; DB 2; Length 214;  
Best Local Similarity 28.6%; Pred. No. 2.2e-09;  
Matches 53; Conservative 48; Mismatches 74; Indels 10; Gaps 4;  
QY 59 RVILGPPASGKTTIAMWLCKHNSLLTLENI---LNEFSYTATEARLYLQRTKTPS 115  
D 2 RIILLGAPGAGGTQAOQFIMEKYGIPQISTGDMLEAAVKAAGSELGKAKEIMDAGKLVTD 61  
QY 116 ALLVQLIERLAEDCIKQWILDGIPETREQALRIQTILGTPRHVIVLSAPDVLIERN 175  
D 62 ELVIALVKERITQEDC-RDGLDGFPTTQADAKKEAGIKVDYVLEFVDFVDELIVERI 120  
QY 176 LGRKIDPDTGRIYHTTFDWEPESEION-----RLAVPEDISELTAQKLEYHNRVVI 230  
D 121 VGRVHAASGRVHVKEN-PPKVEDKDDVTGELTIKDDQDQATVRKRLLEYHQQTAPLV 179  
QY 231 PSYPK 235

Mon Mar 21 09:11:08 2005

A;Residues: 1-215 <GLA>  
 A;Cross-references: UNIPROT:Q927M8; GB:AL592022; PIDN:CA97986.1; PID:gl6415296; GSPDB:GN  
 A;Experimental source: strain Clp11262  
 C;Genetics:  
 A;Gene: adk  
 C;Superfamily: adenylate kinase

Db 180 SYHK 184

## RESULT 14

KIHUA3

nucleoside-triphosphate-adenylate kinase (EC 2.7.4.10) 3 - human

N;Alternate names: adenylate kinase 3

C;Species: Homo sapiens (man)

C;Date: 17-Apr-1993 #sequence\_revision 23-Mar-1995 #text\_change 09-Jul-2004

C;Accession: A16380; S16381

R;Xu, G.; O'Connell, P.; Stevens, J.; White, R.

Genomics 13, 537-542, 1992

A;Title: Characterization of human adenylate kinase 3 (AK3) cDNA and mapping of the AK3

A;Reference number: A42820; MUID:92347846; PMID:1639383

A;Accession: A42820

A;Molecule type: mRNA

A;Residues: 1-223 &lt;XUG&gt;

A;Cross-references: UNIPROT:P27144; EMBL:X60673; NID:928576; PIDN:CAA43088.1; PID:928577

A;Experimental source: frontal-cortex

A;Note: sequence extracted from NCBI backbone (NCBIN:109644, NCBIP:109645)

C;Comment: This isozyme is found in the mitochondrial matrix.

C;Genetics:

A;Gene: GDB:AK3

A;Cross-references: GDB:118988; OMIM:103030

A;Map position: 9pter-9p13

C;Function:

A;Description: catalyzes the reversible phosphorylation of adenine monophosphate with nu

A;Note: GTP is preferred to ATP as a substrate

C;Superfamily: adenylate kinase

C;Keywords: ATP; mitochondrial matrix; mitochondrion; P-loop; phosphotransferase

F;12-19/Region: nucleotide-binding motif A (P-loop) #status atypical.

F;85-89/Region: nucleotide-binding motif B #status atypical

F;22,33,58/Active site: Cys, His, Ser, Asp #status predicted

Query Match 9.6%; Score 240; DB 1; Length 223;

Best Local Similarity 29.6%; Pred. NO. 2.3e-09;

Matches 66; Conservative 45; Mismatches 88; Indels 24; Gaps 7;

QY 270 RVLILGPVSGKSLQAALLAOKYRLVNVCCQLLKEAVADRTTFGELIQPFPEKEMAVPD 329

Db 7 RAVILGPVSGSGTVCQRIQNFGLHLSGHFLRENKASTVEGEMAKQYIEKSLVDP 66

QY 330 SLIMKVLSQLDQDCIQK--WVLHGVPRDLQAHNLRLGYNPNRVFFLNVFPDSIME 387

Db 67 HVITRLMSELEN---RRGQHWLDGFPRTLQGAELDKI-CEVDLVISLNIPFETLK 121

QY 388 RUTLRIDPVTGERHYLMKPPPTMEIQ----ARLLQNPDAEEQVKLMDLFYRNSADL 443

Db 122 RLSRRWIHPSPGRVYNLDFNPHVHGIDDVTCGEPLVQEDDKPEAVARLRQYKDVAKPV 181

QY 444 EOLYGSAILT---NGDQD-----PYTVPEYIESGIINPLPKK 477

Db 182 IELYKRGVHLHQFSGTETNKIWPVYVTLF-----SNKITPIQSK 220

## RESULT 15

AB1777

adenylate kinases homolog adk [imported] - Listeria innocua (strain Clp11262)

C;Species: Listeria innocua

C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004

C;Accession: AB1777

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker

; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma

ok, C.; Schlueter, T.; Simoes, N.; Trierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AB1777

A;Status: preliminary

A;Molecule type: DNA

Query Match 9.5%; Score 237; DB 2; Length 215;

Best Local Similarity 28.7%; Pred. NO. 3.6e-09;

Matches 60; Conservative 50; Mismatches 87; Indels 12; Gaps 5;

QY 270 RVLILGPVSGKSLQAALLAOKYRLVNVCCQLLKEAVADRTTFGELIQPFPEKEMAVPD 329

Db 2 KLVLMGLPGAGRGTAQEQIVKYNIPHISTGDMFRAAMKNNTELGGKAKSPMDGDLVDP 61

QY 330 SLIMKVLSQLDQDCIQK--WVLHGVPRDLQAHNLRLGYNPNRVFFLNVFPDSI 385

Db 62 EVTNGIVRELAEDDA-KNGFLLDGFPRTVQABELENIILSDLTGTELDVAVINIEVDKDLV 120

QY 386 MERLTLRIDPVTGERHYLMKPPPT---MEIQ-ARLLQNPDAEEQVKLMDLFYRNSA 441

Db 121 MKRLTGRWICRTGKTYHEIYNPPKVPCKCDLDDGELYQREDDKKETVENELNVNMKQTK 180

QY 442 DLEQLY---GSAITLNGDQDPVTVPEYIE 467

Db 181 PLLDFYSEKGLHSINGEQINDVFDVDE 209

Search completed: March 18, 2005, 15:21:33

Job time : 44 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 18, 2005, 15:08:37 ; Search time 181 seconds  
(without alignments)  
1355.171 Million cell updates/sec

Title: US-10-798-773-2

Perfect score: 2500

Sequence: 1 MDATAPHRIPPEMPQYGE.....YTVPEYIESGIINLPKPKIP 479

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2500	100.0	479	2 Q96MA6	Q96ma6 homo sapien
2	2008	80.3	479	2 Q68FP8	Q68fp8 rattus norv
3	1429	57.2	275	2 Q8N9W9	Q8n9w9 homo sapien
4	1409	56.4	485	2 Q6F618	Q6f618 xenopus tro
5	372.5	14.9	290	2 Q6ZC69	Q6zc69 oryza sativ
6	364.5	14.6	293	1 KADD_ARATH	Q6fij7 arabidopsis
7	363.5	14.5	222	1 KADD_MAIZE	P43188 zea mays (m
8	363.5	14.5	260	2 Q6Y8Q6	Q6y8q6 trypanosoma
9	342	13.7	269	2 Q8N910	Q8n910 leishmania
10	333.5	13.3	588	2 Q8VY11	Q8vy11 arabidopsis
11	320	12.8	217	2 Q9FY07	Q9fy07 arabidopsis
12	313.5	12.5	260	2 Q6QT32	Q6qt32 trypanosoma
13	292	11.7	221	1 KAD_THETN	Q8v7x4 thermotoma
14	288	11.5	215	1 KAD_OCEIH	Q8etw3 oceanobacil
15	286	11.4	260	2 Q7YUN3	Q7yuns trypanosoma
16	281	11.2	212	1 KAD_STRMU	Q6ds33 streptococc
17	279.5	11.2	217	2 Q64A66	Q64a66 uncultured
18	279	11.2	211	1 KAD_FUSNN	Q8re31 fusobacteri
19	277	11.1	216	1 KAD_CLOTE	Q7p5x4 fusobacteri
20	275	11.0	211	2 Q7P5X4	Q7p5x4 fusobacteri
21	274	11.0	217	1 KAD_ARCFU	Q29581 archaeoglob
22	273	10.9	212	1 KAD_STRPN	Q97sul streptococc
23	272	10.9	212	1 KAD_STRR6	Q8rd44 streptococc
24	272	10.9	217	1 KAD_BACHD	P38372 bacillus ba
25	271	10.8	220	2 Q62HI0	Q62hi0 streptococ
26	271	10.8	220	2 Q63WL6	Q63wl6 burkholderi
27	268	10.7	219	2 Q6FD71	Q6fd71 acinetobact
28	260	10.4	215	1 KAD_CLOAB	Q37ej9 clostridium
29	260	10.4	216	2 Q73F75	Q73f75 bacillus ce
30	259	10.4	212	1 KAD_STRPY	P82549 streptococc
31	258	10.3	212	1 KAD_STRAS	P65203 streptococc

32	258	10.3	212	1 KAD_STRAS	P65204 streptococc
33	258	10.3	212	1 KAD_STRP3	Q8k8x1 streptococc
34	258	10.3	212	1 KAD_STRP8	Q9p224 streptococc
35	258	10.3	216	1 KAD_BACCR	Q81j22 bacillus ce
36	258	10.3	218	1 KAD_CLOPE	Q8xhu4 clostridium
37	257.5	10.3	214	1 KAD_VIBCH	Q9ktb7 vibrio chol
38	257	10.3	216	2 Q67JW4	Q67jw4 symbiobacter
39	257	10.3	220	1 KAD_GLOVI	O7nkt5 symbiobacter
40	256.5	10.3	209	1 KAD_TRYBR	O61069 trypanosoma
41	256.5	10.3	218	1 KAD_BORPE	P39068 bordetella
42	255.5	10.2	206	1 KAD_AOUAE	O66490 aquifex aeo
43	255.5	10.2	218	1 KAD_BORBR	O7wku8 bordetella
44	255.5	10.2	218	1 KAD_BORPA	Q7wgo bordetella
45	252.5	10.1	214	1 KAD_VIBVU	Q8dfmi vibrio vuln

## ALIGNMENTS

### RESULT 1

Q96MA6 PRELIMINARY; PRT; 479 AA.  
AC Q96MA6; 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Hypothetical protein FLJ32704 (Chromosome 9 open reading frame 98).  
GN Name=C9orf98;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC ISSUES=Testis;  
RX PubMed=14702039; DOI=10.1038/ng1285;  
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Sekine M., Ohyashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Yamamoto J., Saito K., Iwayanagi T., Wagatsuma M., Shiratori K., Murakami K., Yasuda T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y., Abe K., Kamiyama K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Tanai H., Kimata M., Watanabe M., Hirsoaka S., Chiba Y., Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hotuta T., Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura J., Togashi S., Komai F., Hara R., Takeuchi K., Arita M., Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S., Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O., Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hiro M., Ohmori Y., Kawabata A., Hikiji T., Kobatake N., Inegaki H., Ikema Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;  
RT "Complete sequencing and characterization of 21,243 full-length human cDNAs.";  
RL Nat. Genet. 36:40-45 (2004).  
[2]  
RP SEQUENCE FROM N.A.  
RN TISSUE=Brain;  
RC MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,



QY 121 LIOBLAEEDCIKQWILGDPETREOALRIOTLGTTPRHVIVLSAPDVTIERNLGKRI 180  
Db 121 LVQRLNEDDCIARGWILGDPETREOALRIOTLGTTPRHVIVLSAPDVTIERNLGKRI 180  
QY 181 DPOTGIYHTTMDPPESEIQRNLWVPEDISELETAQKLEYHNRVIVPSYKILKVI 240  
Db 181 DPTGIEYHTTMDPPESEIQRNLWVPEDISELETAQKLEYHNRVIVPSYKILKVI 240  
QY 241 SADQPCVDVYQALTYVQSNHRTNAPTPRVLLGPGVSGKSLQAALLAOKYRLVNVCCG 300  
Db 241 SSDQPCVDVYQALTYVQSNHRTNAPTPRVLLGPGVSGKSLQAALLAOKYRLVNVCCG 300  
QY 301 QLLKEAVADRTTFFGLIOPPEPEKEMAVPDSLLMKVLSQRLDQDCIQKGVHLGVPDRDLD 360  
Db 301 QLLKEAVADRTTFFGLIOPPEPEKEMAVPDSLLMKVLSQRLDQDCIQKGVHLGVPDRDLD 360  
QY 361 QALLNRLGYNPNRVFLNVPFDSIMERLTLRIDPVTGERHLMYKPPPTMEIOARLLQ 420  
Db 361 QALLNRLGYNPNRVFLNVPFDSIMERLTLRIDPVTGERHLMYKPPPTMEIOARLLQ 420  
QY 421 NPKDAEBOVKMLDLYRNSADLEQLYGSAITLNGDQDPTVTFYIESGIINPLPKKI 478  
Db 421 NPKDSEYIKLQTLDFYRNSADLEQLYGSAITLNGDQDPTVTFYIESGIINPLPKKI 478

## RESULT 3

Q8N9W9 PRELIMINARY; PRT; 275 AA.  
ID Q8N9W9  
AC Q8N9W9  
DT 01-OCT-2002 (TRENBLrel. 22, Created)  
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
DE Hypoetical protein FLJ36127.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RC TISSUE=Testis;  
RP SEQUENCE FROM N.A.  
RX PubMed=14702039; DOI=10.1038/ngl1285;  
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
RA Wakamatsu A., Havaashi K., Sato H., Nagai K., Kimura K., Makita H.,  
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,  
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,  
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,  
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,  
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,  
RA Tanai H., Kimata M., Watanabe M., Hiraoaka S., Chiba Y., Ishida S.,  
RA Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hota T., Kusano J.,  
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,  
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,  
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,  
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shionhara N., Sano S.,  
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,  
RA Yanazaki M., Watanabe K., Kumagai A., Itakura S., Fukutami Y.,  
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,  
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,  
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
RA Okitani R., Wakakami T., Noguchi S., Itoh T., Shigetani K., Senba T.,  
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
RA Mizushima-Sugano J., Satoh N., Kikuchi H., Masuho Y., Yamashita R.,  
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,  
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugeno S.,  
RT "Complete sequencing and characterization of 21,243 full-length human  
RT cDNAs.";  
RL Nat. Genet. 36:40-45(2004).

-I- SIMILARITY: Belongs to the adenylate kinase family.  
CC EMBL; AK093446; BAC04168.1; -.  
DR HSP; P43188; 1ZAK.  
DR CO; GO:0005524; F:ATP binding; IEA.  
DR CO; GO:0016301; F:kinase activity; IEA.  
DR CO; GO:0016740; F:transferase activity; IEA.  
DR InterPro; IPR000850; Adenylate\_kin.  
DR Pfam; PF00406; ADK; 1.  
DR PRINTS; PR00094; ADENYLTKNASE.  
DR ProDom; PD000657; Adenylate\_kin; 1.  
DR Kinase; Transferase.  
SQ SEQUENCE 275 AA; 31455 MW; B90C76CF137D6C34 CRC64;  
Query Match 57.2%; Score 1429; DB 2; Length 275;  
Best Local Similarity 100.0%; Pred. No. 1.8e-85;  
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 205 MYPEDISELETAQKLEYHNRVIVPSYKILKVISADQPCVDVYQALTYVQSNHRTN 264  
Db 1 MYPEDISELETAQKLEYHNRVIVPSYKILKVISADQPCVDVYQALTYVQSNHRTN 60  
QY 265 APPTFRVLLGPGVSGKSLQAALLAOKYRLVNVCCGQLLKEAVADRTTFFGLIOPPEKE 324  
Db 61 APPTFRVLLGPGVSGKSLQAALLAOKYRLVNVCCGQLLKEAVADRTTFFGLIOPPEKE 120  
QY 325 MAVPDSLLMKVLSQRLDQDCIQKGVHLGVPDRDLDQAHLLNRLGYNPNRVFLNVPFDS 384  
Db 121 MAVPDSLLMKVLSQRLDQDCIQKGVHLGVPDRDLDQAHLLNRLGYNPNRVFLNVPFDS 180  
QY 385 IMERLTLRIDPVTGERHLMYKPPPTMEIOARLLQNPDAEQVKLQMDLYRNSADLE 444  
Db 181 IMERLTLRIDPVTGERHLMYKPPPTMEIOARLLQNPDAEQVKLQMDLYRNSADLE 240  
QY 445 QLYGSAITLNGDQDPTVTFYIESGIINPLPKIP 479  
Db 241 QLYGSAITLNGDQDPTVTFYIESGIINPLPKIP 275

## RESULT 4

Q8P618 PRELIMINARY; PRT; 485 AA.  
ID Q8P618  
AC Q8P618  
DT 05-JUL-2004 (TRENBLrel. 27, Created)  
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
DE Hypoetical protein MGC76170.  
GN Names=MGC76170;  
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8364;  
RN [1]  
RC TISSUE=Embryo;  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Haefl N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haefl F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Rana S.S., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[2]

SEQUENCE FROM N.A.

TISSUE=Embryo;

Klein S., Gerhard D.S.; Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.

-1- SIMILARITY: Belongs to the adenylyate kinase family.

EMBL; BC062516; AAH62516.1; -.

HSSP; P05082; 1AKE.

DR GO:0005524; F:ATP binding; IEA.

DR GO:0008603; F:AMP-dependent protein kinase regulator act. .; IEA.

DR GO:0007165; P:signal transduction; IEA.

DR GO:0007165; P:signal transduction; IEA.

DR InterPro; IPR000850; Adenylyate\_kin.

DR InterPro; IPR003117; RIIa.

DR Pfam; PF00406; ADK; 2.

DR PRINTS; PR00094; ADENYLTKINASE.

DR ProDom; PD000657; Adenylyate\_kin; 2.

KW Hypothetical protein; Kinase; Transferase.

SEQUENCE 485 AA; 54786 MW; C2810A7C1EBBAD6C CRC64;

Query Match 56.4%; Score 1409; DB 2; Length 485;

Best Local Similarity 54.1%; 98; Pred. No. 7.5e-84;

Matches 259; Conservative Indels 0; Gaps 0;

QY 1 MDATIAHRIPPEPQYGEENHIFELMQNMLEQLLIHQEPDIPFMFQHLHRDNDVPRI 60

DB 1 MDATRKPLRIPPAMALYAEQGVFDIIQKQWVLYVDPRKDPQIQYMDIHLSNDNDVPRV 60

QY 61 VILGPPASGKTTIAMWLCKHNSLLTLENILNEFSYTAEARRLYLQRTVPSALLVQ 120

DB 61 FILGPPASGKHTMAKLLCRNLNATHLTPTESVLSDDVSLAKEAQSRYDKQGEVDELWAK 120

QY 121 LIQRLABEDCIKQWILDGIPETREQALRIQTGITPRHVIVLSAPDTVLIERNLGRKI 180

DB 121 LMQQLRSKVDCKIKRGWILEGFPKTRREQALQKLMAGICPDHLVLDAPDIVLIERNMGRKI 180

QY 181 DPQCEIYVHTTQWDFWPESEIQNRLMVPRDISELETAQKLEVHRNIVAVIPSPKILKVI 240

DB 181 PTANGEVYHTTDFDWPSPDPTQVRLVPEPGISEETGLRLIEVHRNIPGLRTYPTKTSKKI 240

QY 241 SADQPCVDVYQALTYVQSNHRTNAPFTPRVLLLLGPGVSGKSLQALLAQKVLVNVCCG 300

DB 241 NADQPMVDVFSQVLTIFVLCKPSRLAPHTPRILLYGGPGSGRSLQASLLAQKYGIVNICG 300

QY 301 QLLKEAVDRTTFGLIOPFFKEWAVPDSLMLKVLRSORLQDQCICQKGWVLHGVPRLD 360

DB 301 QVLKEAVADQTKLGEVIQYPIENDQQVDPNLVILKILTEHLSLESATHGWVLHGFPDRTD 360

QY 361 QAHLNRLGYNPNRVFFLVNPPFDSIMERITLRRIDPVTGERVHLMKPPPTTWEIQARLIQ 420

DB 361 QAALLKADAGFVNPVFSLDSDVDVIERLSLQMTDVPVSGERYHDYIKPAPSEVHERLQQ 420

QY 421 NPKDAEEQVKLMDLYFRNSADLEQLYGSAILTNGQDPTVTFYETESGIIINPLPKKIP 479

DB 421 NPRHSQRVQARLDMDYHANAEEUDEFYDPDVHINADQDPTVTFEFIESYTVSPFLPRLP 479

RESULT 5

Q6ZC69 PRELIMINARY; PRT; 290 AA.

AC Q6ZC69

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Putative adenylyate kinase, chloroplast (ATP-AMP transphosphorylase).

DE Name=F0007D08.12;

OS Oryza sativa [Japonica cultivar-group].

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzoideae; Oryza.

QX	NCBI_TaxID=39947;
QY	[1]
DB	SEQUENCE FROM N.A.
QY	Sasaki T., Matsumoto T., Yamamoto K.;
DB	Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
QY	-1- SIMILARITY: Belongs to the adenylate kinase family.
DB	EMBL; AP004584; BAD09526.1; --
QY	HSSP; P05082; IAKE
DB	GO; GO:0005524; F:ATP binding; IEA.
QY	GO; GO:0016301; F:kinase activity; IEA.
DB	GO; GO:0016776; F:phosphotransferase activity; IEA.
QY	GO; GO:0016740; F:transferase activity; IEA.
DB	InterPro; IPR000850; Adenylate_kin.
QY	InterPro; IPR006259; Adenyl_kin_sub.
DB	Pfam; PF00406; ADK; 1
QY	PRINTS; PR00094; ADENYLTKNASE
DB	ProDom; PD000657; Adenylate_kin; 1.
QY	TIGRFAMs; TIGR01351; adk; 1.
DB	PROSITE; PS00113; ADENYLATE_KINASE; 1.
QY	Kinase; Transferase.
DB	SEQUENCE 290 AA; 31816 MW; 058918D67A71E8D2 CRC64;
QY	Query Match 14.9%; Score 372.5; DB 2; Length 290;
DB	Best Local Similarity 34.3%; Pred. No. 2e-16;
QY	Matches 86; Conservative 41; Mismatches 99; Indels 25; Gaps 3;
DB	228 RVIPSPKILKVIADGPDVDFYQALTYVOSNHNAPTRPRVLLGLPVGSKSLQAL 287
QY	57 RSLPRAAKVVAVKAD-----PL--KWTAGAPASGKGTQCEL 92
DB	288 LAQKRLNVNCGQLLKEAVADRTTFCGLIQPFPEKEMAVPDSLMLKVLSDQLDQDCIQ 347
QY	93 IKSXYGLVHISAGDILRAIISAAAGSENGKRAKEFMKGQLVPDEIVNVNKKELLPDAQE 152
DB	348 KGWLVHGVPRDLDDQAHLLNRLGYNPNRVFFLNVPFDSIMERLTLRIDPVTGERHLMYK 407
QY	153 KGWLLDGYPRSYSONMALETNIRPDIFILLDVPDELLVERVVGRRLLDPVTGKIYHLKYS 212
DB	408 PPTTMEIQARLLQNPFDABEQVKLMDLFFNSADLEQLYGSAIT-LNGDQDPYTVFEVI 466
QY	213 PPENEBIASRLTQRFDTEEKVKLRLOTHYQNVESLLSIYEDVIVEKGDALVDDVFAEL 272
DB	467 ESGIINPLPKK 477
QY	273 DKOLTSLSLQK 283
DB	STANDARD; PRT; 283 AA.
QY	RESULT 6
DB	KADD_ARATH
QY	ID KADD_ARATH
DB	AC Q9FIJ7;
QY	DT 10-OCT-2003 (Rel. 42, Created)
DB	DT 25-OCT-2003 (Rel. 42, Last sequence update)
QY	DT 25-OCT-2004 (Rel. 45, Last annotation update)
DB	DE Probable adenylate kinase 2, chloroplast precursor (EC 2.7.4.3) (ATP-
QY	DE AMP transphosphorylase).
DB	GN OrderedLocustNames=At5G47840; ORFNames=MCA23.18;
QY	OS Arabidopsis thaliana (Mouse-ear cress).
DB	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
QY	OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
DB	OC eucoids II; Brassicales; Brassicaceae; Arabidopsids.
QY	OX NCBI_TaxID=3702;
DB	[1]
QY	SEQUENCE FROM N.A.
DB	RC STRAIN=sv. Columbia;
QY	RX MEDLINE=9915233; PubMed=10048488;
DB	RA Asanizu E., Sato S., Kaneko T., Nakamura Y., Kotani H., Miyajima N.,
QY	RA Tabata S.;
DB	RT "Structural analysis of Arabidopsis thaliana chromosome 5. VIII.
QY	RT Sequence features of the regions of 1,081,958 bp covered by seventeen
DB	RT physically assigned pl and TAC clones.";
QY	RN DNA Res. 5:3179-391(1998).
DB	[2]

```

RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;
RA Yanada K., Kim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Miranda M., Quach H.B., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Anesari Y.,
RA Arakawa T., Barth J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
RA Hayao O., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.P.,
RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
RA Khan S., Koesena E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
RA Satou M., Tames R., Vayenberg M., Wallender E.K., Wong C., Yamamura Y.,
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Empirical analysis of transcriptional activity in the Arabidopsis
RL genome.";
RL Science 302:842-846 (2003).
CC -!- FUNCTION: This small ubiquitous enzyme is essential for
CC maintenance and cell growth (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + AMP = 2 ADP.
CC -!- SUBCELLULAR LOCATION: Chloroplast (By similarity).
CC -!- SIMILARITY: Belongs to the adenylate kinase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB016886; BAB11331.1; -
DR EMBL; AY049305; AAK83647.1; -
DR EMBL; E1001036; AAM46790.1; -
DR HSP; P43188; 12AK.
DR InterPro; IPR006259; Adenyl_kin_sub.
DR InterPro; IPR000850; Adenylate_kin.
DR Pfam; PF00406; ADK; 1.
DR PRINTS; PR00094; ADENYLTKINASE.
DR PRODOM; PD000657; Adenylate_kin; 1.
DR TIGRFAMs; TIGR01351; adk; 1.
DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
DR ATP-binding; Chloroplast; Kinase; Transferase; Transit peptide.
FW CHAIN 1 59 Chloroplast (potential).
FT NP BIND 60 283 Probable adenylate kinase 2.
FT NP BIND 71 79 ATP (By similarity).
SQ SEQUENCE 283 AA; 31452 MW; 1461D1A36F2DF4E9 CRC64;

Query Match 14.6%; Score 364.5; DB 1; Length 283;
Best Local Similarity 36.4%; Pred. No. 6.4e-16;
Matches 76; Conservative 39; Mismatches 93; Indels 1; Gaps 1;

OY 270 RVLLGPGVSGSLQAALLAOKYRLVNVCGQLLKEAVADRTTFGELLQPFKEKMAVDP 329
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
66 KIMISGAPASGKGTQCELLTHYGLVHISAGDLLRAEIASGSENGRRAKEHNGQLVDP 125
OY 330 SLAMKVLSQLDQDCIOKGWLVHGVPRDLQAHLLNRLGYNPNKRVFELNVPFDSIMERL 389
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
126 EIVVMVAVKRLSDTSEQGLWLLDGYPRASQATKLGFGQFDLFVLEVPBEILIERV 185
OY 390 TLRIIDPVTGERHYLMYKPPPTMEIQARLQNPDAEQVCLKMDFYRNSADLEQLYGS 449
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
186 VGRRLDPVTGKYHLKYSPPETELAVRLTORPFDTEKAKLRLKTHNQNSVDLSNYDD 245
OY 450 -AITLNGDQDPVTVFVIESGIINPLPKK 477
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:
246 ITIKIEGNRSKEEVEFAQIDSSLSSELLQER 274

RESULT 7
KADC MAIZE
ID_KADC_MAIZE STANDARD; PRT; 222 AA.

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AC P43188;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE Adenylate kinase, chloroplast (EC 2.7.4.3) (ATP-AMP
DE transphosphorylase).
GN Name=ADKI;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Leaf;
RX MEDLINE=94298837; PubMed=8026505;
RA Schiltz E., Burger S., Grafmuller R., Deppert W.R., Haehnel W.,
RA Wagner E.;
RT "Primary structure of maize chloroplast adenylate kinase.";
RL Eur. J. Biochem. 222:949-954 (1994).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).
RX MEDLINE=98089957; PubMed=9428681;
RA Wild K., Grafmuller R., Wagner E., Schulz G.E.;
RT "Structure, catalysis and supramolecular assembly of adenylate kinase
RT from maize.";
RL Eur. J. Biochem. 250:326-331 (1997).
CC -!- FUNCTION: This small ubiquitous enzyme is essential for
CC maintenance and cell growth. The maize enzyme also works with CMP,
CC albeit with 10% of the activity with AMP.
CC -!- CATALYTIC ACTIVITY: ATP + AMP = 2 ADP.
CC -!- SUBCELLULAR LOCATION: Chloroplast.
CC -!- MASS SPECTROMETRY: MW=24867; METHOD=Electrospray; RANGE=1-222;
CC NOIS=ref.1.
CC -!- SIMILARITY: Belongs to the adenylate kinase family.
DR PIR; S45634; S45634.
DR PDB; 1ZAK; X-ray; A/B=1-222.
DR MaizeDB; 13836; -.
DR InterPro; IPR006259; Adenyl_kin_sub.
DR InterPro; IPR000850; Adenylate_kin.
DR Pfam; PF00406; ADK; 1.
DR PRINTS; PR00094; ADENYLTKINASE.
DR PRODOM; PD000657; Adenylate_kin; 1.
DR TIGRFAMs; TIGR01351; adk; 1.
DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
KW 3D-structure; ATP-binding; Chloroplast; Direct protein sequencing;
KW Kinase; Transferase.
FT NP BIND 12 20 ATP (By similarity).
FT STRAND 8 12
FT TURN 14 15
FT HELIX 18 29
FT STRAND 32 33
FT HELIX 36 46
FT TURN 47 47
FT HELIX 49 59
FT TURN 60 61
FT HELIX 66 78
FT HELIX 80 84
FT TURN 85 85
FT TURN 87 90
FT STRAND 96 103
FT TURN 104 106
FT STRAND 111 116
FT HELIX 119 126
FT TURN 127 128
FT STRAND 129 131
FT TURN 133 135
FT STRAND 138 140
FT STRAND 150 154
FT HELIX 156 156
FT STRAND 159 160
FT TURN 163 164
FT TURN 165 165
FT HELIX

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Db 41 HLLRPPQIVIAAGPPGSGKGTCCQAIVRFGVWHISSGDLIRAEVAAAGTEVGKMAET 100  
 Qy 320 FFEKEMAVPDSLLMKVLSQRLDOQDCIOKGWLVGVPRDLDDQAHLLNRLGYNPNRVFFLN 379  
 Db 101 FIHNGEMVFNKIVISAVRKRLEQDDVVKERGWLLDQGFPSQDQAEALSSGIVPHVFLLE 160  
 Qy 380 VPDSIMERLTLRRIDPVTGRIYHLMYKPPPTMEIQ--ARLLQNPDAEBOVKLMDLFY 437  
 Db 161 VPTIVVEIENRRTDPATGMVYHLLYNPPPPEDVALCERLIQRDDHRETVEARLIYH 220  
 Qy 438 RNSADLEQLYGSAI-TLNGDQDPYTFE 464  
 Db 221 EKLHGLKEHYGLTVETINGDQSIHATVE 248  
 RESULT 9  
 QN9N10 PRELIMINARY; PRT; 269 AA.  
 ID Q9N910  
 AC Q9N910; (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Possible adenylate kinase.  
 GN Name=16294.05;  
 OS Leishmania major.  
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
 OX NCBI\_TaxID=5664;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Friedlin;  
 RX MEDLINE=98146435; PubMed=9477341;  
 RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,  
 RA Smith D.F.;  
 RT "A physical map of the Leishmania major Friedlin genome.";  
 RL Genome Res. 8:135-145(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Friedlin;  
 RA Hilbert H., Wedler H., Wedler E., Duesterhoeft A., Ivens A.C.,  
 RA Quail M., Rajandream M.A., Barrell B.G.;  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the adenylate kinase family.  
 DR EMBL; AL354533; CAB89615.1; --  
 DR HSSP; P05082; 1ZAK.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0016301; F:kinase activity; IEA.  
 DR GO; GO:0016776; F:phosphotransferase activity, phosphate grou. .; IEA.  
 DR GO; GO:0015740; F:transferase activity; IEA.  
 DR InterPro; IPR000850; Adenylate kin.  
 DR InterPro; IPR006259; Adenyl\_kin\_sub.  
 DR Pfam; PF00406; ADK; 1.  
 DR PRINTS; PR00094; ADENYLTKNASE.  
 DR TIGRFAMs; TIGR01351; adk; 1.  
 DR PROSITE; PS00113; ADENYLATE\_KINASE; 1.  
 KW Kinase; Transferase.  
 SQ SEQUENCE 269 AA; BAB658834D6984E1 CRC64;  
 Query Match 13.7%; Score 342; DB 2; Length 269;  
 Best Local Similarity 31.3%; Pred. No. 1.8e-14;  
 Matches 81; Conservative 54; Mismatches 104; Indels 20; Gaps 6;  
 Qy 17 YGRENHIFELMQLFELIHOPEDPFPMIOHLHRDNDNVPRIVLGPPASGKTTAMW 76  
 Db 14 YIKDNIGQLMEVILRCIITDKPTKPLEYV--HELTASLPFPRVVLGPPASGKGTQARH 71  
 Qy 77 LCK-----HLNS-SALTLEMLINRFSYATEARLYLQKTVPSALVQLIQE 124  
 Db 72 ICYSYKRAIKGKPVHVHSGDGLRAE----VAQTHGLKTAENFMQRGELVPDSLIIIRN 128  
 Qy 125 RLAEEDCICKWGLDIPETREQALRIOTLTPRHVIVLSAPDTVLIERNLGKIDPQT 184  
 Db 129 RLQTEDAVNMGWLLDGPFRTRSQALDAALDAAGLCPRIFVYLDTPDDVLFGRVEGRDPT 188

TURN 183 184  
 STRAND 188 192  
 HELIX 197 219  
 TURN 220 220  
 SEQUENCE 222 AA; 24867 MW; 19257324F8B7630D CRC64;  
 Query Match 14.5%; Score 363.5; DB 1; Length 222;  
 Best Local Similarity 37.3%; Pred. No. 5.5e-16;  
 Matches 78; Conservative 40; Mismatches 90; Indels 1; Gaps 1;  
 Qy 270 RYLLGPNVSGKSLQAALLAOKYILNVCCGQLLKEAVADRITFGELIQFFFEKEMAVDP 329  
 Db 7 KUMISGAPASGKGTQCELIKTKYQLAHISAGDLLRAISAGSENGKRAKFEKVGQLVDP 66  
 Qy 330 SLLMKVLSQRLDOQDCIOKGWLVGVPRDLDDQAHLLNRLGYNPNRVFFLNVPDSIMERL 389  
 Db 67 EIVNVNKRLEQPDQAENGWLLDGYPRYSQMALETLEIRPDTFTLLDVPDELIVERV 126  
 Qy 390 TLRRIDPVTGERIYHLMYKPPPTMEIQARLLQNPDAEBOVKLMDLFYRNSADLEQLYGS 449  
 Db 127 VGRLLDPVTGKIYHLKYSPENEEIASLTQRFDDTBKVKRLRTFYIYQNIIESLLTYEN 186  
 Qy 450 AIT-LNGDQDPYTVREYIESGIINPLPKK 477  
 Db 187 IIVKVGDTAVDAVFAKIDELGSLLEKK 215  
 RESULT 8  
 Q6Y8Q6 PRELIMINARY; PRT; 260 AA.  
 ID Q6Y8Q6  
 AC Q6Y8Q6; 2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Adenylate kinase.  
 GN Name=Adek1;  
 OS Trypanosoma cruzi.  
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
 OX NCBI\_TaxID=5693;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CL Brener;  
 RA Bouvier L.A., Miranda M.R., Canepa G.E., Pereira C.A.;  
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the adenylate kinase family.  
 DR EMBL; AY169824; AA013019.1; --  
 DR HSSP; P05082; 1AKE.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0016301; F:kinase activity; IEA.  
 DR GO; GO:0016776; F:phosphotransferase activity, phosphate grou. .; IEA.  
 DR GO; GO:0015740; F:transferase activity; IEA.  
 DR InterPro; IPR000850; Adenylate kin.  
 DR InterPro; IPR006259; Adenyl\_kin\_sub.  
 DR InterPro; IPR007862; ADK\_lid.  
 DR Pfam; PF00406; ADK; 1.  
 DR Pfam; PF05191; ADK\_lid; 1.  
 DR PRINTS; PR00094; ADENYLTKNASE.  
 DR ProDom; PD000657; Adenylate\_kin; 1.  
 DR TIGRFAMs; TIGR01351; adk; 1.  
 DR PROSITE; PS00113; ADENYLATE\_KINASE; 1.  
 KW Kinase; Transferase.  
 SQ SEQUENCE 260 AA; BBCE886E43115F8C CRC64;  
 Query Match 14.5%; Score 363.5; DB 2; Length 260;  
 Best Local Similarity 30.6%; Pred. No. 6.7e-16;  
 Matches 82; Conservative 53; Mismatches 106; Indels 27; Gaps 5;  
 Qy 200 IQNRLMVPEIDISELTAQKLELYHRNIVRIPSPKILKVISADQPCDVVFQALTYQS 259  
 Db 5 LDKL---EYLQKHNIAQLTEHVRNIMEDLPENP-----IKV--- 40  
 Qy 260 NHTNAPFTVRLLGPNVSGKSLQAALLAOKYILNVCCGQLLKEAVADRITFGELIQP 319

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QY 185 GIIYHTTDMPESE--IQNLMVPEDISELETAQKLEVHRNIVRIPSYKILKVISA 242
Db 189 GIIYHLKNNPPENDTALLERLQHRDDDTREVLGRLETHSHVWEGLLDYSGIMYHVDG 248
QY 243 DQPCVDVFOYQALTYVQSNH 261
Db 249 NRPEAAITKDITEYLO-NH 266

RESULT 10
Q8VYL1 PRELIMINARY; PRT; 588 AA.
AC Q8VYL1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 05-JUL-2004 (TrEMBLrel. 20, Last sequence update)
DE Putative adenylate kinase.
GN Name=At5g35170;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsia.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayaehizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.-J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Deng J.M., Heuan V.W.,
RA Lee J.M., Quach H.L., Tang C., Toriumi M., Wu H.C., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayaehizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.-J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the adenylate kinase family.
DR EMBL; A1070456; AAM49859.1; -.
DR EMBL; AY133763; AAM91697.1; -.
DR HSSP; P43188; 1ZAK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016776; F:phosphotransferase activity, phosphate grou. .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR Pfam; PF00406; ADK; 1.
DR PRINTS; PR00094; ADENYLTKNASE.
DR ProDom; PD000657; Adenylate_kin; 1.
DR TIGRFAMs; TIGR01351; adk; 1.
DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
KW Kinase; Transferase.
SQ SEQUENCE 588 AA; 65738 MW; 3AA0B81ABFC4B62B CRC64;

Query Match 13.3%; Score 333.5; DB 2; Length 588;
Best Local Similarity 33.7%; Pred. No. 1.7e-13;
Matches 68; Conservative 47; Mismatches 84; Indels 3; Gaps 2;

QY 264 NAPPPTPVLILGPGSGKSIQAALLAQKYLNVNCCQLLKEAVADRTTFGLIOPFEK 323
Db 77 NEPL--KVMISGAPSGKGTQCELIYVHKFGLVHISTGDLRAEVSSGTDIGKRAKEFVNS 134
QY 324 ENAVPDDLKMKVLSQRDQDCIQKGWLVHGVPRDLQAHLNRLGNPNRVFFLNVPFD 383
Db 135 GSLVDPDEIVTAMVAGRLSREDAKEHGWLDDGFPSPFAQSLDKLVNKPDIIFILLDVPDE 194
QY 384 SIMERLTLRRIDPVTGERHYLMYKPPPTWEIQARLLQNPKDAEQVKLWDLFYRNSADL 443

RESULT 11
Q9FY07 PRELIMINARY; PRT; 217 AA.
AC Q9FY07;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Adenylate kinase-like.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsia.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA Tabata S.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the adenylate kinase family.
DR EMBL; AP000421; BAB10023.1; -.
DR HSSP; P43188; 1ZAK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016776; F:phosphotransferase activity, phosphate grou. .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR000850; Adenylate_kin.
DR InterPro; IPR006259; Adenyl_kin_sub.
DR Pfam; PF00406; ADK; 1.
DR PRINTS; PR00094; ADENYLTKNASE.
DR ProDom; PD000657; Adenylate_kin; 1.
DR TIGRFAMs; TIGR01351; adk; 1.
DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
KW Kinase; Transferase.
SQ SEQUENCE 217 AA; 24065 MW; 76FBED1964ACD04E CRC64;

Query Match 12.8%; Score 320; DB 2; Length 217;
Best Local Similarity 34.4%; Pred. No. 3.7e-13;
Matches 62; Conservative 42; Mismatches 76; Indels 0; Gaps 0;

QY 272 LLLGPGVSGKSLQAALLAQKYLNVNCCQLLKEAVADRTTFGLIOPFEKMAVPDSL 331
Db 1 MISGAPSGKGTQCELIYVHKFGLVHISTGDLRAEVSSGTDIGKRAKEFVNSGSLVPEI 60
QY 332 LMKVLSQRDQDCIQKGWLVHGVPRDLQAHLNRLGNPNRVFFLNVPFDSIMERLTL 391
Db 61 VIAMVAGRLSREDAKEHGWLDDGFPSPFAQSLDKLVNKPDIIFILLDVPDEILDRCVG 120
QY 392 RRIDPVTGERHYLMYKPPPTWEIQARLLQNPKDAEQVKLWDLFYRNSADLQYCSAI 451
Db 121 RRLDPVTGKIYHKNYPPESEDEIKARLVTRPDTEKVKARLIQYKQNSEAISAYSDVM 180

RESULT 12
Q6QT32 PRELIMINARY; PRT; 260 AA.
AC Q6QT32;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Adenylate kinase 4.
GN Name=Adk4;
OS Trypanosoma cruzi.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5693;
RN [1]
RP SEQUENCE FROM N.A.

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Db 195 ILIDRCVGRRLDPVTGKIYHKNYPPESEDEIKARLVTRPDTEKVKARLIQYKQNSEAI 254
QY 444 EQYGS-A-ITLNGDOOPVTYFE 464
Db 255 ISAYSDVMVKIDANRPKEVWFE 276

RESULT 11
Q9FY07 PRELIMINARY; PRT; 217 AA.
AC Q9FY07;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Adenylate kinase-like.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsia.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA Tabata S.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the adenylate kinase family.
DR EMBL; AP000421; BAB10023.1; -.
DR HSSP; P43188; 1ZAK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016776; F:phosphotransferase activity, phosphate grou. .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR000850; Adenylate_kin.
DR InterPro; IPR006259; Adenyl_kin_sub.
DR Pfam; PF00406; ADK; 1.
DR PRINTS; PR00094; ADENYLTKNASE.
DR ProDom; PD000657; Adenylate_kin; 1.
DR TIGRFAMs; TIGR01351; adk; 1.
DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
KW Kinase; Transferase.
SQ SEQUENCE 217 AA; 24065 MW; 76FBED1964ACD04E CRC64;

Query Match 12.8%; Score 320; DB 2; Length 217;
Best Local Similarity 34.4%; Pred. No. 3.7e-13;
Matches 62; Conservative 42; Mismatches 76; Indels 0; Gaps 0;

QY 272 LLLGPGVSGKSLQAALLAQKYLNVNCCQLLKEAVADRTTFGLIOPFEKMAVPDSL 331
Db 1 MISGAPSGKGTQCELIYVHKFGLVHISTGDLRAEVSSGTDIGKRAKEFVNSGSLVPEI 60
QY 332 LMKVLSQRDQDCIQKGWLVHGVPRDLQAHLNRLGNPNRVFFLNVPFDSIMERLTL 391
Db 61 VIAMVAGRLSREDAKEHGWLDDGFPSPFAQSLDKLVNKPDIIFILLDVPDEILDRCVG 120
QY 392 RRIDPVTGERHYLMYKPPPTWEIQARLLQNPKDAEQVKLWDLFYRNSADLQYCSAI 451
Db 121 RRLDPVTGKIYHKNYPPESEDEIKARLVTRPDTEKVKARLIQYKQNSEAISAYSDVM 180

RESULT 12
Q6QT32 PRELIMINARY; PRT; 260 AA.
AC Q6QT32;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Adenylate kinase 4.
GN Name=Adk4;
OS Trypanosoma cruzi.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5693;
RN [1]
RP SEQUENCE FROM N.A.

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Mon Mar 21 09:11:08 2005

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CC STRAIN=CL Brenner;
CC Bouvier L.A., Miranda M.R., Canepa G.E., Pereira C.A.;
CC Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the adenylate kinase family.
CC EMBL; AYS26734; AAS20418.1; -.
CC DR HSSP; P05082; IAKE.
CC DR GO; GO:0005524; F:ATP binding; IEA.
CC DR GO; GO:0016301; F:kinase activity; IEA.
CC DR GO; GO:0016740; F:transferase activity; IEA.
CC DR InterPro; IPR000850; Adenylate_kin.
CC DR Pfam; PF00406; ADK; 1.
CC DR PRINTS; PR00094; ADENYLTKNASE.
CC DR ProDom; PD000657; Adenylate_kin; 1.
CC DR Kinase; Transferase.
CC KW SEQUENCE 260 AA; OCCAG7290386081F CRC64;
CC
CC Query Match 12.5%; Score 313.5; DB 2; Length 260;
CC Best Local Similarity 30.2%; Pred. No. 1.2e-12;
CC Matches 73; Conservative 52; Mismatches 108; Indels 9; Gaps 5;
CC
CC QY 17 YGEENHIFELMQLLEQLIHOPEDPFPFMIQHLHRDNDNPRIVILGPPASGKTTIAMW 76
CC Db ||||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
CC QY 13 YFEKHINTLEELPHDVMVLPDLPLOLHAL--DRKTLRLMVLGSGAGKRTQSR 70
CC Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC QY 77 LCKHLNSSLLENLILNEFSYTAERRL--YLQRTKVPSSALLVOLIQERLAEDCIK 133
CC Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC QY 71 IAKGVAVVNNADVPREMSKETKEGVANCMREGIPVPHDVASELILRLKVEDANS 130
CC Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC QY 134 QGWILDGIPETREQALRIQTGLTPRHVIVLSADPTVLIERNLGRIDPQTGEIYHTTFD 193
CC Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
CC QY 131 NGWVLNGPRTSEALRLQTAGISPLFTLLDLPYENAVQRCNGRYDPIPTQNYHMEFC 190
CC Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC QY 194 WPPESEIQRLMVPED-ISELETAQKLEYHNRIVRVPSPKILKVISADQPCVDVIFYQ 252
CC Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
CC QY 191 PPPEGNAVERMFEDDDSLAASVSRWKFYDARKD--ELIECEYFVVRIDGNRP-VDVVSQ 247
CC Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC QY 253 AL 254
CC Db 248 EI 249
CC
CC RESULT 13
CC KAD THETN STANDARD; PRT; 221 AA.
CC AC Q8R7X4; 2003 (Rel. 41, Created)
CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
CC DT 25-OCT-2004 (Rel. 45, Last annotation update)
CC DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
CC GN Name=adk; OrderedLocuNames=TTE2271;
CC OS Thermoanaerobacter tengcongensis.
CC OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
CC OC Thermoanaerobacteriaceae; Thermoanaerobacter.
CC OX NCBI_TaxID=119072;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=MB4 / JCM 11007;
CC RX MEDLINE=21992816; PubMed=11997336; DOI=10.1101/gr.219302;
CC RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
CC RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
CC RA Tan H., Chen K., Wang J., Yu J., Yang H.;
CC RA "A complete sequence of the T. tengcongensis genome.";
CC RL Genome Res. 12:689-700(2002).
CC CC -1- FUNCTION: This small ubiquitous enzyme is essential for
CC CC maintenance and cell growth.
CC CC -1- CATALYTIC ACTIVITY: ATP + AMP = 2 ADP.
CC CC -1- SUBUNIT: Monomer (By similarity).
CC CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC CC -1- SIMILARITY: Belongs to the adenylate kinase family.
CC
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CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; AEO13171; AM25415.1; -.
CC DR HSSP; P27142; IZIN.
CC DR HAMAP; MF 00235; -.
CC DR InterPro; IPR006259; Adenyl_kin_sub.
CC DR InterPro; IPR000850; Adenylate_kin.
CC DR InterPro; IPR007862; ADK_lid.
CC DR Pfam; PF00406; ADK; 1.
CC DR Pfam; PF05191; ADK_lid; 1.
CC DR PRINTS; PR00094; ADENYLTKNASE.
CC DR ProDom; PD000657; Adenylate_kin; 1.
CC DR TIGRFAMs; TIGR01351; adk; 1.
CC DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
CC DR ATP-binding; Complete proteome; Kinase; Transferase.
CC KW NP_BIND 7 15 ATP (By similarity).
CC FT SEQUENCE 221 AA; B19D5675CE8B33E7 CRC64;
CC
CC Query Match 11.7%; Score 292; DB 1; Length 221;
CC Best Local Similarity 28.6%; Pred. No. 2.6e-11;
CC Matches 61; Conservative 61; Mismatches 79; Indels 12; Gaps 4;
CC
CC QY 270 RVLLIGPVSGSKLQAAALLAOKYRLVNVCCQLLKEAVADRTTFGLIQPFPEKEMAVPD 329
CC Db 2 RVLLIGPVGAGGQALAKIKEFDIPHISTGDIIFQNLRDNTLGLKLAKEYMDKGLLVPD 61
CC QY 330 SLIMKVLSQLDQDCIQKGVNLHGVPRDLDOAHLNRL-----GYNPNRVFFLAVPDSI 385
CC Db 62 EVTNRIREDLEKEDC-KKGFLLDGYPNIPQAEELDFLEERGHSLTAVINIQVERAL 120
CC QY 386 MERLTLLRRIDPTGYERYHLMYKPPPTMEI-----QARLLQNPQDAEEQVKLQKDLFYRNSA 441
CC Db 121 IDRITGRRYPCVCGATYHKTSPKVDNVCCKGSELQSRDDKLESVVKLEVVYKETK 180
CC QY 442 DLEQLY---GSAITLNGDQDPYTVFYIESGII 471
CC Db 181 PLIDYTKGILVNIIDGNKSIDVEFDIKKALL 213
CC
CC RESULT 14
CC KAD OCEIH STANDARD; PRT; 215 AA.
CC AC Q8ETW3;
CC DT 10-OCT-2003 (Rel. 42, Created)
CC DT 10-OCT-2003 (Rel. 42, Last sequence update)
CC DT 25-OCT-2004 (Rel. 45, Last annotation update)
CC DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
CC GN Name=adk; OrderedLocuNames=OB0140;
CC OS Oceanobacillus iheyensis.
CC OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
CC OX NCBI_TaxID=182710;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=HTE831 / DSM 14371 / JCM 11309;
CC RX MEDLINE=2220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
CC RA Takami H., Takaki Y., Uchiyama I.;
CC RA "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
CC RA Ridge and its unexpected adaptive capabilities to extreme
CC RA environments.";
CC RL Nucleic Acids Res. 30:3927-3935(2002).
CC CC -1- FUNCTION: This small ubiquitous enzyme is essential for
CC CC maintenance and cell growth.
CC CC -1- CATALYTIC ACTIVITY: ATP + AMP = 2 ADP.
CC CC -1- SUBUNIT: Monomer (By similarity).
CC CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC CC -1- SIMILARITY: Belongs to the adenylate kinase family.
CC
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
-----

DR EMBL; AP004593; BAC12096.1; -  
DR HSSP; P27143; IZIN.  
DR HAMAP; MF\_00735; 1.  
DR InterPro; IPR000850; Adenylate\_kin.  
DR InterPro; IPR006259; Adenylate\_kin\_sub.  
DR InterPro; IPR007862; ADK\_lid.  
DR Pfam; PF00406; ADK; 1.  
DR Pfam; PF05151; ADK\_lid; 1.  
DR PRINTS; PR00094; ADENYLKINASE.  
DR PROSITE; PS00035; Adenylate\_kin; 1.  
DR PROSITE; PS00113; ADENYLATE\_KINASE; 1.  
DR KINASE; KINASE; 1.  
KW ATP-binding; Complete proteome; Kinase; Transferase.  
FT NE\_BIND 7 15 ATP (By similarity).  
SQ SEQUENCE 215 AA; 24064 MW; 14DEFCE27364E03 CRC64;

Query Match 11.5%; Score 288; DB 1; Length 215;  
Best Local Similarity 33.0%; Pred. No. 4.5e-11;  
Matches 69; Conservative 46; Mismatches 82; Indels 12; Gaps 4;  
QY 271 VLLGPGVSGKSLQAALLAOKYRLVNVCCGQLLKEAVADRTTFGELIQPFKEKEMAVPDS 330  
DB 3 LILMLGPGAGKGTAAKINEKYNIPHISTGDMFLRAIKETGLCKAKERFMDGDLVPDE 62  
QY 331 LLMKVLSQLQDQDCIQKGMVLHGVPRLDQA---HLNRLGYNPNRVFFLNVPDSTM 386  
DB 63 VTGVGVKERLAMDDC-ANGFLDGFPTTRQAEELQNLSDLGKSIDYVHVDVPEKLV 121  
QY 387 ERLTLRRIDPVTGERYHLMYKPPPTMEI---QARLLQNPDAEQVKLMDLFYNSAD 442  
DB 122 ERLTGRICPTCGTAYHVYVNPKEGICDKDGSQIQDQDDQPTVKNRLAVNIEQTQP 181  
QY 443 LEQLY---GSAITLNGDQDPTVTFVIES 468  
DB 182 LLDFFQDKGVLVKVNGDRDINVVFQDIES 210

## RESULT 15

Q7YUN3 PRELIMINARY; PRT; 260 AA.  
ID Q7YUN3  
AC Q7YUN3  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Adenylate kinase.  
GN ORFNames=TB927.2.5660;  
OS Trypanosoma brucei  
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
OX NCBI\_TaxID=5691;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=2789169; PubMed=12907728; DOI=10.1093/nar/gkg673;  
RA El-Sayed N.M.A., Ghedin E., Song J., MacLeod A., Bringaud F.,  
RA Larkin C., Haniss D., Peterson J., Hou L., Taylor S., Tweedie A.,  
RA Bateau N., Khatek H.G., Lin X., Mason T., Hannick L., Caler E.,  
RA Blandin G., Bartholomeu D., Simpson A.J., Kaul S., Zhao H., Pai G.,  
RA Van Aken S., Ueberback T., Haas B., Koo H.L., Umayam L., Suh B.,  
RA Gerard C., Leach V., Qi R., Zhou S., Schwartz D., Feldblyum T.,  
RA Salzbeg S., Tait A., Turner M.R., Ullu E., White O., Melville S.,  
RA Adams M.B., Fraser C.M., Donelson J.E.;  
RT The sequence and analysis of Trypanosoma brucei chromosome II.;  
RT Nucleic Acids Res. 31:4856-4863(2003).  
CC [- SIMILARITY: Belongs to the adenylate kinase family.  
DR EMBL; AE017170; AAQ16024.1; -  
DR HSSP; P05082; IE4Y.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0016301; F:kinase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.

DR InterPro; IPR000850; Adenylate\_kin.  
DR Pfam; PF00406; ADK; 1.  
DR ProDom; PD000657; Adenylate\_kin; 1.  
KW Kinase; Transferase.  
SQ SEQUENCE 260 AA; 29339 MW; 8F15B485E68B1FC7 CRC64;  
Query Match 11.4%; Score 286; DB 2; Length 260;  
Best Local Similarity 27.2%; Pred. No. 7.8e-11;  
Matches 67; Conservative 51; Mismatches 116; Indels 12; Gaps 4;  
QY 233 YPKILKVISADOPCVDFVQALTYVQSNHRTNAPTPRVLVLLGPGVSGKSLQAALLAOKY 292  
DB 21 FEQIVQNIISDAP-----ERPMSYIGDLMRRGIPL--QIFTAGPAGSGKRTOCKNTADRL 73  
QY 293 RLNVVCCGQLLKEAVADRTTFGELIQPFKEKEMAVPDSLLMKVLSQRLDQDQDCIQKGMVL 352  
DB 74 GVVLSSGQVLTGRGVESGSETSQLAHSYVSRGERVPTLVSMIMKDLRLSQSDAREKGMVL 133  
QY 353 HGVTPLDQAHLLNRLGYNPNRVFFLNVPDSTMERLTLLRRIDPVTGERYHLMYKPPPTM 412  
DB 134 EGYPRNAQQAQAVEECGVIPQVFIILLDFELSPRLEHRRYDPATNKSYHMLNDNPPAE 193  
QY 413 EIQ--ARLLQNPDAEQVKLMDLFYNSADLEQLYGSATLNGDQDPTVTFVIESGI 470  
DB 194 DVALCERLVORDADPFHESIAKLAQYIESIEGVKKHLGAVIEV---VDARKSVEDVERDI 250  
QY 471 INPLPK 476  
DB 251 LAAVEK 256

Search completed: March 18, 2005, 15:20:44  
Job time : 183 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 18, 2005, 15:11:03 ; Search time 49 Seconds  
(without alignments)  
729.733 Million cell updates/sec

Title: US-10-798-773-2  
Perfect score: 2500  
Sequence: 1 MDATIAPHRIPPEMPQVGESE.....YTVFEYIESGIINLPKPKIP 479

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgm2\_6/ptodata/1/aaa/5A.COMB.pbp.\*  
2: /cgm2\_6/ptodata/1/aaa/5B.COMB.pbp.\*  
3: /cgm2\_6/ptodata/1/aaa/5A.COMB.pbp.\*  
4: /cgm2\_6/ptodata/1/aaa/5B.COMB.pbp.\*  
5: /cgm2\_6/ptodata/1/aaa/PTUS.COMB.pbp.\*  
6: /cgm2\_6/ptodata/1/aaa/backfiles.pbp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2500	100.0	479	US-10-141-634-2	Sequence 2, Appli
2	491	19.6	94	US-10-141-634-4	Sequence 4, Appli
3	280.5	11.2	222	US-09-328-352-5675	Sequence 5675, Ap
4	273	10.9	212	US-09-583-110-4124	Sequence 4124, Ap
5	273	10.9	216	US-09-107-433-4765	Sequence 4765, Ap
6	249	10.0	66	US-09-513-999C-7572	Sequence 7572, Ap
7	247.5	9.9	222	US-09-134-001C-3289	Sequence 3289, Ap
8	242.5	9.7	215	US-09-710-279-1580	Sequence 1580, Ap
9	240	9.6	223	US-08-829-027-5	Sequence 5, Appli
10	240	9.6	223	US-09-225-366-5	Sequence 5, Appli
11	240	9.6	273	US-09-949-016-9245	Sequence 9245, Ap
12	238	9.5	225	US-09-489-039A-12712	Sequence 12712, A
13	236.5	9.5	223	US-09-543-681A-7057	Sequence 7057, Ap
14	233.5	9.3	227	US-08-829-027-3	Sequence 3, Appli
15	233.5	9.3	227	US-09-225-366-3	Sequence 3, Appli
16	233	9.3	282	US-09-252-991A-21097	Sequence 21097, A
17	231.5	9.3	227	US-09-149-476-377	Sequence 377, App
18	228.5	9.1	227	US-08-829-027-1	Sequence 1, Appli
19	228.5	9.1	227	US-09-225-366-1	Sequence 1, Appli
20	225.5	9.0	179	US-09-540-236-3142	Sequence 3142, Ap
21	220.5	8.8	227	US-08-829-027-4	Sequence 4, Appli
22	220.5	8.8	227	US-09-225-366-4	Sequence 4, Appli
23	214.5	8.6	240	US-09-134-000C-5802	Sequence 5802, Ap
24	212	8.5	237	US-09-949-016-10565	Sequence 10565, A
25	208.5	8.3	217	US-09-438-185A-246	Sequence 246, App
26	208.5	8.3	217	US-09-438-185A-246	Sequence 246, App
27	198.5	7.9	231	US-09-107-532A-3675	Sequence 3675, Ap

ALIGNMENTS

RESULT 1  
US-10-141-634-2  
; Sequence 2, Application US/10141634  
; Patent No. 6734010  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Xuanchuan  
; APPLICANT: Xie, Qionghu  
; APPLICANT: Abuin, Alejandro  
; APPLICANT: Walker, D. Wade  
; TITLE OF INVENTION: No. 6734010el Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0344-USA  
; CURRENT APPLICATION NUMBER: US/10/141.634  
; PRIOR FILING DATE: 2002-05-08  
; PRIOR APPLICATION NUMBER: US 60/289,727  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 479  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-141-634-2

Query Match	100.0%	Score	2500;	DB	4;	Length	479;
Best Local Similarity	100.0%	Pred. No.	4.4e-251;				
Matches	479;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MDATIAPHRIPPEMPQVGEENHIFELMQLLIHQPEDIPPMIOHLHRDNDNVPRI	60				
Db	1	MDATIAPHRIPPEMPQVGEENHIFELMQLLIHQPEDIPPMIOHLHRDNDNVPRI	60				
Qy	61	VILGPPASGKTTIAMWLCKHNSLLTLENLINESFSTATEARLYLQKTVPSALLVQ	120				
Db	61	VILGPPASGKTTIAMWLCKHNSLLTLENLINESFSTATEARLYLQKTVPSALLVQ	120				
Qy	121	LIOERLAEEDCIKQWILDCIPETREQALRIOTLGIPTPRHIVLSAPDTVLIERNLGKRI	180				
Db	121	LIOERLAEEDCIKQWILDCIPETREQALRIOTLGIPTPRHIVLSAPDTVLIERNLGKRI	180				
Qy	181	DPQTEIYHTTDFMPPSEIQRNLMPVEDISELETAQKLEYHNRNIVRVIPSPKILKVI	240				
Db	181	DPQTEIYHTTDFMPPSEIQRNLMPVEDISELETAQKLEYHNRNIVRVIPSPKILKVI	240				
Qy	241	SADQPCVDVFOALTYVQSNHRTNAPFTPRVLLIGFVGSGKSLQALLAKYLVNVC	300				
Db	241	SADQPCVDVFOALTYVQSNHRTNAPFTPRVLLIGFVGSGKSLQALLAKYLVNVC	300				
Qy	301	QLLKEAVADRTTCGELIQPFKEKMAVPSLIMKVLSDLDQDCIQKGVHLGVPRDLD	360				
Db	301	QLLKEAVADRTTCGELIQPFKEKMAVPSLIMKVLSDLDQDCIQKGVHLGVPRDLD	360				

361 QAHLNRLGYNPNRFFLNVPFDSIMERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQ 420  
361 QAHLNRLGYNPNRFFLNVPFDSIMERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQ 420  
421 NPKDAEQVKLMDLFYRNSADLEBQLYGSAITLNGDDPVTVEYIESGLINPLPKIP 479  
421 NPKDAEQVKLMDLFYRNSADLEBQLYGSAITLNGDDPVTVEYIESGLINPLPKIP 479

RESULT 2  
US-10-141-634-4  
; Sequence 4, Application US/10141634  
; Patent No. 6734010  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Xuanchuan  
; APPLICANT: Xie, Qiongshu  
; APPLICANT: Abuin, Alejandro  
; APPLICANT: Walke, D. Wade  
; TITLE OF INVENTION: No. 6734010e1 Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0344-USA  
; CURRENT APPLICATION NUMBER: US/10/141.634  
; CURRENT FILING DATE: 2002-05-08  
; PRIOR APPLICATION NUMBER: US 60/289,727  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 94  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-141-634-4

Query Match 19.6%; Score 491; DB 4; Length 94;  
Best Local Similarity 100.0%; Pred. No. 3.2e-43; Indels 0; Gaps 0;  
Matches 94; Conservative 0; Mismatches 0

386 MERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQPKDAEQVKLMDLFYRNSADLEQ 445  
1 MERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQPKDAEQVKLMDLFYRNSADLEQ 60

446 LYGSAILTNGDDPVTVEYIESGLINPLPKIP 479  
61 LYGSAILTNGDDPVTVEYIESGLINPLPKIP 94

RESULT 3  
US-09-328-352-5675  
; Sequence 5675, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 5675  
; LENGTH: 222  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-5675

Query Match 11.2%; Score 280.5; DB 4; Length 222;  
Best Local Similarity 29.6%; Pred. No. 9.8e-21;  
Matches 66; Conservative 47; Mismatches 93; Indels 17; Gaps 5;

267 FTFRVLLGPGVGSKSLQAALLAQKYLNVNCGQLLKEAVADRTTFGELIQPFPEKEWA 326  
4 FFWRIILGPGGAGKTQAQKIVQEHVAHISTGDMFRAMANOTEMGLAKSYIDKGLVLPDE 63  
327 VPDSLLMKVLSQRLDQDCIQKGWLVHGVPRDLQAHLLNRLGYNPNRFFLNVPFDSIM 386

64 VSDLIILGLVKERIAQDCV-NGCIFDGFRTTIPQAALEKSGISIDHVIIDVPDEIV 122  
387 ERLTLRRIDPVTGERYHLMYKPPPTM-----EIQARLLQPKDAEQVKLMDLFYRNSAD 442  
123 KRLSGRRQHPASGRVYHVYVNPFPKVEGKDDTGTGDLVQRDDQETIRKGLASVH---TE 179  
443 LEQLYG--SAITLNGDDP-----YTVFEYIESGLINPLPK 476  
180 TEQLVFGVYOGRAASGENAPTYDKLDGLRTIEDVQKDLFNILDK 222

RESULT 4  
US-09-583-110-4124  
; Sequence 4124, Application US/09583110  
; Patent No. 6699703  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al.  
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus  
; FILE REFERENCE: Pneumoniae for Diagnostics and Therapeutics  
; CURRENT APPLICATION NUMBER: US/09/583,110  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/107,433  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/085,131  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: US 60/051,553  
; PRIOR FILING DATE: 1997-07-02  
; NUMBER OF SEQ ID NOS: 5322  
; SEQ ID NO 4124  
; LENGTH: 212  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-09-583-110-4124

Query Match 10.9%; Score 273; DB 4; Length 212;  
Best Local Similarity 31.6%; Pred. No. 5.5e-20;  
Matches 67; Conservative 46; Mismatches 85; Indels 14; Gaps 4;

271 VLLGPGVGSKSLQAALLAQKYLNVNCGQLLKEAVADRTTFGELIQPFPEKEWAVPDS 330  
3 LLTMGLPGAGKTQAQKIVQEHVAHISTGDMFRAMANOTEMGLAKSYIDKGLVLPDE 62  
331 LLMKVLSQRLDQDCIQKGWLVHGVPRDLQAHLLNR-----LGYNPNRFFLNVPFDSIM 386  
63 VTNGIVKERLSQDDIKETGFLDGYRTTIEQAHLDKTLAELGIELEGVINIEVNPDSLL 122  
387 ERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQPKDAEQVKLMDLFYRNSADLEQL 446  
123 ERLSGRIIHRVTGTFHKVFNPPVDYK-BEDYYQREDDKPTVKRDLV---NIAQGEPI 178  
447 Y-----GSAITLNGDDPVTVEYIESGLIN 472  
179 IAHYRAKGLVHDIEGNDINDVFSDEIKVLTN 210

RESULT 5  
US-09-107-433-4765  
; Sequence 4765, Application US/09107433  
; Patent No. 6800744  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID  
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE  
; THERAPEUTICS  
; NUMBER OF SEQUENCES: 5206  
; CORRESPONDENCE ADDRESS:  
; ADDRESSSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA





us-10-798-773-2.ra1

Mon Mar 21 09:11:07 2005

FILING DATE: Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0256 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 223 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 28577  
US-08-829-027-5  
Query Match 9.6%; Score 240; DB 2; Length 223;  
Best Local Similarity 29.6%; Pred. No. 1.6e-16;  
Matches 66; Conservative 45; Mismatches 88; Indels 24; Gaps 7;  
QY 270 RYLLGPVSGSKSLQAALLAQKRYLVNVCQQLKEAVADRTTFGELIQPFPEKEMAVPD 329  
DB 7 RAVILGPPGSGKGTVCORIAQNFGLHLSGHFLRENKASTVEGEMAKQYIEKSLIVPD 66  
QY 330 SILMKVLSQRLDQDCIQKG--WVLHGVPRLDQAHNLNRLGYNPNRVFFLNVPFDSIME 387  
DB 67 HWITRLMSELEN-----RQGHWLDGFPRTLQGAELDKI-CEVDLVISLNIPETLKD 121  
QY 388 RLTLRLRIDPVTGERHYLMYKPPPTWEIQ-----ARLLQNPKDAEQQVKLMDLFYENSADL 443  
DB 122 RLSSRWHPGSGRVNLDNPNPHVHGIDDDVTGEPVQQEDDKPEAAARLQYKDVAKPV 181  
QY 444 EQYGSAYTL---NGQD-----PVTPEYIESGIINPLPKK 477  
DB 182 IELYKRGVLHOPSGTETNKWIPYVTLF-----SNKITPIQSK 220  
RESULT 10  
US-09-225-366-5  
Sequence 5, Application US/09225366  
Patent No. 6001624  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Shah, Purvi  
TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/225,366  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/829,027  
FILING DATE:

QY 436 ---FYNSADLEQLYGS 449  
DB 189 ILEYNNKGVKKNIDGS 205  
RESULT 8  
US-09-710-279-1580  
Sequence 5, Application US/09710279  
Patent No. 6703492  
GENERAL INFORMATION:  
APPLICANT: KIMMERLY, WILLIAM JOHN  
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
FILE REFERENCE: P03480US  
CURRENT APPLICATION NUMBER: US/09/710,279  
CURRENT FILING DATE: 2000-11-09  
PRIOR APPLICATION NUMBER: 60/164,258  
PRIOR FILING DATE: 1999-11-09  
NUMBER OF SEQ ID NOS: 4472  
SOFTWARE: Patent in ver. 2.1  
SEQ ID NO 1580  
LENGTH: 215  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
OTHER INFORMATION: amino acid sequence  
US-09-710-279-1580  
Query Match 9.7%; Score 242.5; DB 4; Length 215;  
Best Local Similarity 28.4%; Pred. No. 8.3e-17;  
Matches 56; Conservative 47; Mismatches 75; Indels 19; Gaps 4;  
QY 271 VLLGPVSGSKSLQAALLAQKRYLVNVCQQLKEAVADRTTFGELIQPFPEKEMAVPDS 330  
DB 3 IILGLPGAGKGTQASEIVKKEPIPHISTGDMFRKAIKDETDLGKEAKSYMDRGELVPDE 62  
QY 331 LLMKVLSQLDQDCIQKGWVLHGVPRLDQAHNLNRLGYNPNR-----VFFLNVPFDSIM 386  
DB 63 VTVGIKVERISEDDA-KKGFLDGFPTIDQAESLSQMSELDREIDAVINIEVPEBELM 121  
QY 387 ERLTLRIDPVTGERHYLMYKPPPTWEI-----QARLLQNPKDAEQQVKLMDL----- 435  
DB 122 NRLTGRICEKCGTTHLVFNPKVDGICDIDGGKLYOREDDNPNVSNRLSVNVKQSKP 181  
QY 436 ---FYNSADLEQLYGS 449  
DB 182 ILEYNNKGVKKNIDGS 198  
RESULT 9  
US-08-829-027-5  
Sequence 5, Application US/08829027  
Patent No. 5858160  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Shah, Purvi  
TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/829,027

ATTORNEY/AGENT INFORMATION:  
NAMS: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0256 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 223 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 28577  
US-09-225-366-5

Query Match 9.6%; Score 240; DB 3; Length 223;  
Best Local Similarity 29.6%; Pred. No. 1.6e-16;  
Matches 66; Conservative 45; Mismatches 88; Indels 24; Gaps 7;  
QY 270 RVLLGPGVSGKSLQAALLAOKYRLNVCCGQLLKEAVADRTTFGELIQPFPEKEMAVPD 329  
Db 7 RAVILGPGSGKGTVCORIAQNFGLHSSGHFLRENTKASTEVGENAKQYIEKSLVDP 66  
QY 330 SLLMKVLSQRLDQDCIQKG--WVLHGVRPRDLDDQAHLLNRLGYNPNRVFFLNVPFDSIME 387  
Db 67 HVITRLMSELEN-----RRQHWLLDGFPTLGOAALDKI-CEVDLVISLNIPTFETLKD 121  
QY 388 RLTLRRIDPVTGERHYLMYKPPPTMEIQ-----ARLLQNPKDAEQVKLMDLFYRNSADL 443  
Db 122 RLRSRWIHPPSGRVYNLDNPNPHVHGIDVDVTGEPLVQOEDDKPEAAVRLRQYKQVAPV 181  
QY 444 EQLYGSATL---NGDQD-----PVTVFYIESGINPLPKK 477  
Db 182 IELYKRGVLHQFSGTETNKIWPYVYTLF-----SNKITPQSK 220

## RESULT 11

US-09-949-016-9245  
Sequence 9245, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CLO01307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR FILING DATE: 2000-10-20  
PRIOR FILING DATE: 2000-10-20  
PRIOR FILING DATE: 2000-10-20  
PRIOR FILING DATE: 2000-10-20  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: Fast-Seq for Windows Version 4.0  
SEQ ID NO 9245  
LENGTH: 273  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-9245

Query Match 9.6%; Score 240; DB 4; Length 273;  
Best Local Similarity 29.6%; Pred. No. 2.2e-16;  
Matches 66; Conservative 45; Mismatches 88; Indels 24; Gaps 7;  
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Db 57 RAVILGPGSGKGTVCORIAQNFGLHSSGHFLRENTKASTEVGENAKQYIEKSLVDP 116

QY 330 SLLMKVLSQRLDQDCIQKG--WVLHGVRPRDLDDQAHLLNRLGYNPNRVFFLNVPFDSIME 387  
Db 117 HVITRLMSELEN-----RRQHWLLDGFPTLGOAALDKI-CEVDLVISLNIPTFETLKD 171  
QY 388 RLTLRRIDPVTGERHYLMYKPPPTMEIQ-----ARLLQNPKDAEQVKLMDLFYRNSADL 443  
Db 172 RLRSRWIHPPSGRVYNLDNPNPHVHGIDVDVTGEPLVQOEDDKPEAAVRLRQYKQVAPV 231  
QY 444 EQLYGSATL---NGDQD-----PVTVFYIESGINPLPKK 477  
Db 232 IELYKRGVLHQFSGTETNKIWPYVYTLF-----SNKITPQSK 270

## RESULT 12

US-09-489-039A-12712  
Sequence 12712, Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et. al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709.2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR FILING DATE: 2000-01-27  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 12712  
LENGTH: 225  
TYPE: PRT  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-12712

Query Match 9.5%; Score 238; DB 4; Length 225;  
Best Local Similarity 29.9%; Pred. No. 2.6e-16;  
Matches 56; Conservative 46; Mismatches 75; Indels 10; Gaps 4;  
QY 57 VPRIVILGPPASGKTTIAMLCKHLNLSLLTLENLI---LNEFSVTATEARRLVLRKTV 113  
Db 11 VMRILLGAPGAGKGTQAQFIMEKYGIPIQISTGDMRLRAAVKSGSELGKQAKDMDAGKLV 70  
QY 114 PSALLVOLIOERLAEECDIKOGWLDGIPETREOALRIQTILGTPRHVIVLSAPDTVLIE 173  
Db 71 TDELVIATYKERIAHEDC-RNGFLDGFPTIIPQADAMKEAGITVDYVLEFDVDELIVD 129  
QY 174 RNGLKRIDPQTGEIYHHTFDWPPSEIQN-----RLMVPEIDISELETAQKLEYHRNIVR 228  
Db 130 RIVGRKVAHSGRVYHVKFN-PPKVGKDDVTGEBELTTRKDDQEEETVKKRLVYHOMTAP 188  
QY 229 VIPSYPK 235  
Db 189 LIGYTK 195

## RESULT 13

US-09-543-681A-7057  
Sequence 7057, Application US/09543681A  
Patent No. 6605709  
GENERAL INFORMATION:  
APPLICANT: GARY BRETON  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709.1002-001  
CURRENT APPLICATION NUMBER: US/09/543,681A  
CURRENT FILING DATE: 2000-04-05  
PRIOR FILING DATE: 2000-04-05  
PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 8344  
SEQ ID NO 7057  
LENGTH: 223  
TYPE: PRT  
ORGANISM: Proteus mirabilis  
US-09-543-681A-7057

us-10-798-773-2.ra1

Mon Mar 21 09:11:07 2005

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Query Match          9.5%; Score 236.5; DB 4; Length 223;
Best Local Similarity 28.7%; Pred. No. 3.7e-16;
Matches 54; Conservative 41; Mismatches 82; Indels 11; Gaps 3;

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Db 8 YAMRIILLGAPGAGKGQAOFIKENYIGIPQISTGDMRLRAAVSAGTELGLKAKALMDNGQL 67
Qy 327 VPDLSLLMKVLSQRLLDQDCIQKGVHLGVPRDLDOAHLNRLGYNPNRVFFLNVPPDSIM 386
Db 68 VTDELVALVKERIKQDDC-RNGFLLDGFRTIPQADAMKEAGINVDVLEFAVPDEIIV 126
Qy 387 ERLTRRIDPVTGGRYHLMYKPPPTMEIQAR-----LLQNPQDAEEQVKLMDLIFYRN 439
Db 127 ERIVGRVRHAPSGRYTHIKFNPP---KVENRDVDTGSELTRKDDQDETVRKRLIHYHSQ 183
Qy 440 SADLEQLY 447
Db 184 TAPLVSY 191

RESULT 14
US-08-829-027-3
; Sequence 3, Application US/08829027
; Patent No. 5856160
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,027
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0256 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 217576
; US-08-829-027-3

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Best Local Similarity 30.4%; Pred. No. 7.8e-16;
Matches 59; Conservative 37; Mismatches 81; Indels 17; Gaps 4;

Qy 270 RVLLGPGVSGKSLQAALLAQKYLNVNCGQLLKEAVADRTTFGELIQPFPEKEMAVPD 329
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Db 69 DVMTRLVHELH--KNLTQYNWLLDGFRTLPQAEALDR-AYQIDTVINLNVPEVIKQRL 125
Qy 390 TLRIDPVTGGRYHLMYKPPPTMEIQ-----ARLLQNPQDAEEQVKLMDL----- 435
Db 126 TARWLHFGSGRVYNIENFPKPTMGIDLTGTGPLVQREDDRPETVVKLKA YEATQTEPVL 185
Qy 436 FYRNSADLEQLYGS 449
Db 186 YVRKKGVLTFSGT 199

RESULT 15
US-09-225-366-3
; Sequence 3, Application US/09225366
; Patent No. 6001624
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,366
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/829,027
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0256 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 217576
; US-09-225-366-3

Query Match          9.3%; Score 233.5; DB 3; Length 227;
Best Local Similarity 30.4%; Pred. No. 7.8e-16;
Matches 59; Conservative 37; Mismatches 81; Indels 17; Gaps 4;

Qy 270 RVLLGPGVSGKSLQAALLAQKYLNVNCGQLLKEAVADRTTFGELIQPFPEKEMAVPD 329
Db 9 RAAIMGAPGSGKGVSSRIITKHFELKHLSSGDLRLDNMLRGTEIGVLAKTFIDQKGLIPD 68
Qy 330 SLLMKVLSQRLLDQDCIQKGVHLGVPRDLDOAHLNRLGYNPNRVFFLNVPPDSIMERL 389
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Mon Mar 21 09:11:07 2005

us-10-798-773-2.ra1

Page 7

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QY      390 TLRRIDPVTGERYHLMYKPPPTMEIQ-----ARLLQNPKDABEQVKLKMDL----- 435
Db      126 TARWIIHPSGRVYNIEFNPKTMGIDDLTGEPLVQREDDRPETVVVKRLKAYEAQTEPVL 185
QY      436 FYRNSADLEQLYGS 449
Db      186 YRKGVLTFSGT 199
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Job time : 50 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

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1062.612 Million cell updates/sec

Title: US-10-798-773-2

Perfect score: 2500

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Searched: 1401741 seqs, 330541175 residues

Total number of hits satisfying chosen parameters: 1401741

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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20: /cgn2\_6/ptodata/2/pubaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2500	100.0	479	15	US-10-094-749-3020
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4	1429	57.2	275	15	US-10-104-047-3627
5	1429	57.2	275	15	US-10-311-034-25
6	1301	52.0	258	14	US-10-165-800-22
7	1166	46.6	236	9	US-09-764-868-870
8	553	22.1	113	9	US-09-764-868-868
9	553	22.1	113	9	US-09-764-868-1179
10	491	19.6	94	14	US-10-141-634-4
11	491	19.6	94	17	US-10-798-773-4
12	378.5	15.1	307	15	US-10-424-599-268668
13	372.5	14.9	290	16	US-10-437-963-120944
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Sequence 3627, Ap					
Sequence 25, Appl					
Sequence 22, Appl					
Sequence 870, App					
Sequence 868, App					
Sequence 1179, Ap					
Sequence 4, Appli					
Sequence 4, Appli					
Sequence 268668,					
Sequence 120944,					

14	372	14.9	284	15	US-10-424-599-191515	Sequence 191515,
15	363.5	14.5	303	15	US-10-425-114-47870	Sequence 47870, A
16	363.5	14.5	309	15	US-10-425-114-59931	Sequence 59931, A
17	363.5	14.5	309	15	US-10-425-114-67019	Sequence 67019, A
18	322.5	12.9	310	16	US-10-767-701-43411	Sequence 43411, A
19	293	11.7	801	16	US-10-437-963-172021	Sequence 172021,
20	281	11.2	212	15	US-10-282-122A-72209	Sequence 72209, A
21	278.5	11.1	217	15	US-10-282-122A-44894	Sequence 44894, A
22	273	10.9	212	16	US-10-474-776-612	Sequence 612, App
23	273	10.9	212	17	US-10-472-928-278	Sequence 278, App
24	272	10.9	212	9	US-09-815-242-13219	Sequence 13219, A
25	272	10.9	212	15	US-10-282-122A-73744	Sequence 73744, A
26	271	10.8	220	15	US-10-282-122A-50136	Sequence 50136, A
27	261	10.4	273	15	US-10-425-114-65308	Sequence 65308, A
28	260.5	10.4	220	15	US-10-282-122A-48201	Sequence 48201, A
29	260	10.4	215	15	US-10-282-122A-52019	Sequence 52019, A
30	259	10.4	215	15	US-10-282-122A-74336	Sequence 74336, A
31	259	10.4	241	16	US-10-767-701-43931	Sequence 43931, A
32	257.5	10.3	214	15	US-10-282-122A-77200	Sequence 77200, A
33	256.5	10.3	218	15	US-10-282-122A-51065	Sequence 51065, A
34	255.5	10.2	218	15	US-10-282-122A-63152	Sequence 63152, A
35	253	10.1	271	15	US-10-425-114-58866	Sequence 58866, A
36	253	10.1	271	15	US-10-425-114-60891	Sequence 60891, A
37	252	10.1	216	15	US-10-282-122A-46134	Sequence 46134, A
38	252	10.1	216	15	US-10-282-122A-71311	Sequence 71311, A
39	252	10.1	242	15	US-10-434-599-155349	Sequence 155349, A
40	251	10.0	221	15	US-10-282-122A-53316	Sequence 53316, A
41	249	10.0	260	15	US-10-425-114-61488	Sequence 61488, A
42	248	9.9	218	15	US-10-282-122A-61353	Sequence 61353, A
43	248	9.9	221	15	US-10-282-122A-49618	Sequence 49618, A
44	247	9.9	216	15	US-10-282-122A-52817	Sequence 52817, A
45	247	9.9	227	16	US-10-437-963-172020	Sequence 172020,

ALIGNMENTS

RESULT 1  
US-10-141-634-2  
; Sequence 2, Application US/10141634  
; Publication No. US20030008365A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu Xuanchuan  
; APPLICANT: Xie, Qionghu  
; APPLICANT: Abuin, Alejandro  
; APPLICANT: Mahe, D. Wade  
; TITLE OF INVENTION: No. US20030008365A1el Human Kinases and Polynucleotides Encoding  
; FILE REFERENCE: LEX-0344-USA  
; CURRENT APPLICATION NUMBER: US/10/141.634  
; PRIOR FILING DATE: 2002-05-08  
; PRIOR FILING DATE: 2002-05-08  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 479  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-141-634-2

Query Match 100.0%; Score 2500; DB 14; Length 479;  
Best Local Similarity 100.0%; Pred. No. 1.3e-222;  
Matches 479; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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181 DPQGEIYHTTFDWPPESEIQNRMLWVPEDISELETAQKLELHYHRNIVRVIPSPKILKVI 240
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241 SADQPCVDVFOALTYVQSNHRTNAPPTPRVLLGPGVSGSKSLQAALLAQKYLNVNCCG 300
301 QLLKEAVADRTTFGELIQPFPEKEMAVPDSLLMKVLSQRLDQDCIQKGWLVHGVPRDLD 360
301 QLLKEAVADRTTFGELIQPFPEKEMAVPDSLLMKVLSQRLDQDCIQKGWLVHGVPRDLD 360
361 QAHLNRLGYNPNRVFFLNVPFDSIMERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQ 420
361 QAHLNRLGYNPNRVFFLNVPFDSIMERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQ 420
421 NPKDAEBOVKLMDLFYRNSADLEQLYGSATLNGDQDPYTVFYEIESGIINPLPKKIP 479
421 NPKDAEBOVKLMDLFYRNSADLEQLYGSATLNGDQDPYTVFYEIESGIINPLPKKIP 479

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RESULT 2

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US-10-094-749-3020
; Sequence 3020, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3020
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-3020

```

```

Query Match 100.0%; Score 2500; DB 15; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.3e-222;
Matches 479; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDATIAPHRIPPMPQYGEENHIFELMQNMLEQLLIHQPEDPFPFMIQHLHRDNDVPRI 60
Db 1 MDATIAPHRIPPMPQYGEENHIFELMQNMLEQLLIHQPEDPFPFMIQHLHRDNDVPRI 60
Qy 61 VILGPASGKTTIAMWLCKHNSLLTLENLIINEFSYATATEARRLYLQKTVPSALLVQ 120

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61 VILGPASGKTTIAMWLCKHNSLLTLENLIINEFSYATATEARRLYLQKTVPSALLVQ 120
121 LIQERLAEECDIKQGWILGIPETREQALRIQTLGTPRHVIVLSAPDVTVLERNLGRKI 180
121 LIQERLAEECDIKQGWILGIPETREQALRIQTLGTPRHVIVLSAPDVTVLERNLGRKI 180
181 DPQGEIYHTTFDWPPESEIQNRMLWVPEDISELETAQKLELHYHRNIVRVIPSPKILKVI 240
181 DPQGEIYHTTFDWPPESEIQNRMLWVPEDISELETAQKLELHYHRNIVRVIPSPKILKVI 240
241 SADQPCVDVFOALTYVQSNHRTNAPPTPRVLLGPGVSGSKSLQAALLAQKYLNVNCCG 300
241 SADQPCVDVFOALTYVQSNHRTNAPPTPRVLLGPGVSGSKSLQAALLAQKYLNVNCCG 300
301 QLLKEAVADRTTFGELIQPFPEKEMAVPDSLLMKVLSQRLDQDCIQKGWLVHGVPRDLD 360
301 QLLKEAVADRTTFGELIQPFPEKEMAVPDSLLMKVLSQRLDQDCIQKGWLVHGVPRDLD 360
361 QAHLNRLGYNPNRVFFLNVPFDSIMERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQ 420
361 QAHLNRLGYNPNRVFFLNVPFDSIMERLTLRRIDPVTGERYHLMYKPPPTMEIQARLLQ 420
421 NPKDAEBOVKLMDLFYRNSADLEQLYGSATLNGDQDPYTVFYEIESGIINPLPKKIP 479
421 NPKDAEBOVKLMDLFYRNSADLEQLYGSATLNGDQDPYTVFYEIESGIINPLPKKIP 479

```

RESULT 3

```

US-10-798-773-2
; Sequence 2, Application US/10798773
; Publication No. US20050019885A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Xie, Qiongshu
; APPLICANT: Abuin, Alejandro
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0344-USA
; CURRENT APPLICATION NUMBER: US/10/798,773
; CURRENT FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: US/10/141,634
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/289,727
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 479
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-798-773-2

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Query Match 100.0%; Score 2500; DB 17; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.3e-222;
Matches 479; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDATIAPHRIPPMPQYGEENHIFELMQNMLEQLLIHQPEDPFPFMIQHLHRDNDVPRI 60
Db 1 MDATIAPHRIPPMPQYGEENHIFELMQNMLEQLLIHQPEDPFPFMIQHLHRDNDVPRI 60
Qy 61 VILGPASGKTTIAMWLCKHNSLLTLENLIINEFSYATATEARRLYLQKTVPSALLVQ 120
61 VILGPASGKTTIAMWLCKHNSLLTLENLIINEFSYATATEARRLYLQKTVPSALLVQ 120
Db 61 VILGPASGKTTIAMWLCKHNSLLTLENLIINEFSYATATEARRLYLQKTVPSALLVQ 120
Qy 121 LIQERLAEECDIKQGWILGIPETREQALRIQTLGTPRHVIVLSAPDVTVLERNLGRKI 180
121 LIQERLAEECDIKQGWILGIPETREQALRIQTLGTPRHVIVLSAPDVTVLERNLGRKI 180
181 DPQGEIYHTTFDWPPESEIQNRMLWVPEDISELETAQKLELHYHRNIVRVIPSPKILKVI 240
181 DPQGEIYHTTFDWPPESEIQNRMLWVPEDISELETAQKLELHYHRNIVRVIPSPKILKVI 240
Qy 241 SADQPCVDVFOALTYVQSNHRTNAPPTPRVLLGPGVSGSKSLQAALLAQKYLNVNCCG 300

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Db 241 SADQCVDVYQALTVQSNHRTNAPPTFRVLLGPGVSGKSLQAALLAQKYLNVNCCG 300  
Qy 301 QLLKEAVADRTTFGELIQPFKEKEMAVPDSLLMKVLSORLDQDCIQKGWLVHGVPRDLD 360.  
Db 301 QLLKEAVADRTTFGELIQPFKEKEMAVPDSLLMKVLSORLDQDCIQKGWLVHGVPRDLD 360  
Qy 361 QAHLLNRLGYNPNRVFFLNVPFDSIMERLTLRIDPVTGERVHLMYKPPPTWELQARLLQ 420  
Db 361 QAHLLNRLGYNPNRVFFLNVPFDSIMERLTLRIDPVTGERVHLMYKPPPTWELQARLLQ 420  
Qy 421 NPKDAEQVKLQMDLFYRNSADLEQLYGSALTILNGDQDPTVTFEYESGINPLPKIP 479  
Db 421 NPKDAEQVKLQMDLFYRNSADLEQLYGSALTILNGDQDPTVTFEYESGINPLPKIP 479

## RESULT 4

US-10-104-047-3627  
; Sequence 3627, Application US/10104047  
; Publication No. US20030236392A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA  
; FILE REFERENCE: H1-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; PRIOR FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3627  
; LENGTH: 275  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-104-047-3627

Query Match 57.2%; Score 1429; DB 15; Length 275;  
Best Local Similarity 100.0%; Pred. No. 1e-123;  
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 205 MYPEDISELETAQKLLYHNRNIVRVPSPKILKVISADQPCVDVYQALTYVQSNHRTN 264  
Db 1 MYPEDISELETAQKLLYHNRNIVRVPSPKILKVISADQPCVDVYQALTYVQSNHRTN 60  
Qy 265 APPTFRVLLGPGVSGKSLQAALLAQKYLNVNCCGQLLKEAVADRTTFGELIQPFKE 324  
Db 61 APPTFRVLLGPGVSGKSLQAALLAQKYLNVNCCGQLLKEAVADRTTFGELIQPFKE 120  
Qy 325 MAVPDSLLMKVLSORLDQDCIQKGWLVHGVPRDLDQAHLLNRLGYNPNRVFFLNVPFDS 384  
Db 121 MAVPDSLLMKVLSORLDQDCIQKGWLVHGVPRDLDQAHLLNRLGYNPNRVFFLNVPFDS 180  
Qy 385 IMERLTLRIDPVTGERVHLMYKPPPTWELQARLLQNPDKDAEQVKLQMDLFYRNSADLE 444  
Db 181 IMERLTLRIDPVTGERVHLMYKPPPTWELQARLLQNPDKDAEQVKLQMDLFYRNSADLE 240  
Qy 445 QLYGSALTILNGDQDPTVTFEYESGINPLPKIP 479  
Db 241 QLYGSALTILNGDQDPTVTFEYESGINPLPKIP 275

## RESULT 5

US-10-311-034-25  
; Sequence 25, Application US/10311034  
; Publication No. US20040023242A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: YUE, Henry  
; APPLICANT: LAL, Preeti  
; APPLICANT: BANDMAN, Olga  
; APPLICANT: BOROMSKY, Mark L.  
; APPLICANT: AU-YOUNG, Janice  
; APPLICANT: LU, Yan

APPLICANT: GANDHI, Ameena R.  
APPLICANT: TRIBOULEY, Catherine M.  
APPLICANT: CHAWLA, Narinder K.  
APPLICANT: YAO, Monique G.  
APPLICANT: LU, Dyung Alina M.  
APPLICANT: GREENWALD, Sara R.  
APPLICANT: RAMKUMAR, Jayalaxmi  
APPLICANT: GRIFFIN, Jennifer A.  
APPLICANT: KEARNEY, Liam  
APPLICANT: BURFORD, Neil  
APPLICANT: NGUYEN, Dannel B.  
APPLICANT: TANG, Y. Tom  
APPLICANT: BAUGHN, Mariah R.  
APPLICANT: HE, Ann  
APPLICANT: THORNTON, Michael  
APPLICANT: HAFALIA, April  
APPLICANT: ARVIZU, Chandra S.  
APPLICANT: GURURAJAN, Rajesopal  
APPLICANT: LO, Terence P.  
APPLICANT: KHAH, Farrah A.  
APPLICANT: RECIPON, Shirley A.  
APPLICANT: AZIMZAI, Yalda  
APPLICANT: POLICKY, Jennifer L.  
APPLICANT: DING, Li  
APPLICANT: GREYER, Megan  
APPLICANT: ELLIOTT, Vicki S.  
APPLICANT: THANGAVELU, Kavitha  
APPLICANT: BATRA, Sajeev  
APPLICANT: ISON, Craig H.  
; TITLE OF INVENTION: HUMAN KINASES  
; FILE REFERENCE: PI-0125 PCT  
; CURRENT APPLICATION NUMBER: US/10/311,034  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372,  
; 60/228,056  
; PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-0  
; 25  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PERL Program  
; SEQ ID NO 25  
; LENGTH: 275  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20040023242A1' 621293CD1  
US-10-311-034-25

Query Match 57.2%; Score 1429; DB 15; Length 275;  
Best Local Similarity 100.0%; Pred. No. 1e-123;  
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 205 MYPEDISELETAQKLLYHNRNIVRVPSPKILKVISADQPCVDVYQALTYVQSNHRTN 264  
Db 1 MYPEDISELETAQKLLYHNRNIVRVPSPKILKVISADQPCVDVYQALTYVQSNHRTN 60  
Qy 265 APPTFRVLLGPGVSGKSLQAALLAQKYLNVNCCGQLLKEAVADRTTFGELIQPFKE 324  
Db 61 APPTFRVLLGPGVSGKSLQAALLAQKYLNVNCCGQLLKEAVADRTTFGELIQPFKE 120  
Qy 325 MAVPDSLLMKVLSORLDQDCIQKGWLVHGVPRDLDQAHLLNRLGYNPNRVFFLNVPFDS 384  
Db 121 MAVPDSLLMKVLSORLDQDCIQKGWLVHGVPRDLDQAHLLNRLGYNPNRVFFLNVPFDS 180  
Qy 385 IMERLTLRIDPVTGERVHLMYKPPPTWELQARLLQNPDKDAEQVKLQMDLFYRNSADLE 444  
Db 181 IMERLTLRIDPVTGERVHLMYKPPPTWELQARLLQNPDKDAEQVKLQMDLFYRNSADLE 240  
Qy 445 QLYGSALTILNGDQDPTVTFEYESGINPLPKIP 479  
Db 241 QLYGSALTILNGDQDPTVTFEYESGINPLPKIP 275

Mon Mar 21 09:11:07 2005

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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 870
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (228)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; LOCATION: (234)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-764-868-870

Query Match 46.6%; Score 1166; DB 9; Length 236;
Best Local Similarity 100.0%; Pred. No. 2e-99;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 QALRIQTGTPRHVIVLSAPDTVLIERNLGRKIDPQTGEIYHTTFDWPPESEIQNRLMV 206
DB 1 QALRIQTGTPRHVIVLSAPDTVLIERNLGRKIDPQTGEIYHTTFDWPPESEIQNRLMV 60
QY 207 PEDISELETAQKLEHYHNRVIVPSYKILKVISADQPCVDVVFQALTYVQSHRTNAP 266
DB 61 PEDISELETAQKLEHYHNRVIVPSYKILKVISADQPCVDVVFQALTYVQSHRTNAP 120
QY 267 FTFRVLLGPGVSGKSLQAALLAQKRYLVNVCGLLKEAVADRTTFGELIQPFPEKEMA 326
DB 121 FTFRVLLGPGVSGKSLQAALLAQKRYLVNVCGLLKEAVADRTTFGELIQPFPEKEMA 180
QY 327 VPDSLMLKVLSQLDQDCIQKQWLVHGVPRDLDOAHLNRLGYN 371
DB 181 VPDSLMLKVLSQLDQDCIQKQWLVHGVPRDLDOAHLNRLGYN 225

RESULT 8
US-09-764-868-868
; Sequence 868, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 868
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-764-868-868

Query Match 22.1%; Score 553; DB 9; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.2e-43;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 RVFFLNVPFDSIMERLTLRIDPVTGERYHLMKPPPTMEIQARLLQNPDAEQVKLM 433
DB 8 RVFFLNVPFDSIMERLTLRIDPVTGERYHLMKPPPTMEIQARLLQNPDAEQVKLM 67
QY 434 DLFYRNSADLRLQYSGSAITLNGDDPVTVEYIESGIINPLPKKIP 479
DB 68 DLFYRNSADLRLQYSGSAITLNGDDPVTVEYIESGIINPLPKKIP 113

; Sequence 870, Application US/09764868
; Patent No. US20020168711A1

```

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; GENERAL INFORMATION:
; APPLICANT: Chum, Miyoung
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Meyers, Rachel E.
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Adenylate Kinase, Phospholipid Scramblase-Like, DNA
; TITLE OF INVENTION: Fragmentation Factor-Like, Phosphatidylserine Synthase-Like,
; TITLE OF INVENTION: and ATPase-Like Molecules and Uses Therefor
; FILE REFERENCE: 35800/247838
; CURRENT APPLICATION NUMBER: US/10/165,800
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 09/790,179
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/185,609
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/790,838
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/185,946
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/185,947
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/795,038
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/186,234
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/781,677
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/181,705
; PRIOR FILING DATE: 2000-02-10
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 22
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-165-800-22

Query Match 52.0%; Score 1301; DB 14; Length 258;
Best Local Similarity 99.6%; Pred. No. 6.9e-112;
Matches 253; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 73 IAMWLCKHNSLLTLENLILNEFSYATATARRVLYLQRTVPSALLVOLIQRLAEDCI 132
DB 1 MAMWLCKHNSLLTLENLILNEFSYATATARRVLYLQRTVPSALLVOLIQRLAEDCI 60
QY 133 KQGWILDGIPETREQALRIQTGTPRHVIVLSAPDTVLIERNLGRKIDPQTGEIYHTTF 192
DB 61 KQGWILDGIPETREQALRIQTGTPRHVIVLSAPDTVLIERNLGRKIDPQTGEIYHTTF 120
QY 193 DWPPSEIQNRLMVPDISELETAQKLEHYHNRVIVPSYKILKVISADQPCVDVVFQ 252
DB 121 DWPPSEIQNRLMVPDISELETAQKLEHYHNRVIVPSYKILKVISADQPCVDVVFQ 180
QY 253 ALTVOQSHRTNAPFTFRVLLGPGVSGKSLQAALLAQKRYLVNVCGLLKEAVADRTT 312
DB 181 ALTVOQSHRTNAPFTFRVLLGPGVSGKSLQAALLAQKRYLVNVCGLLKEAVADRTT 240
QY 313 FGELIQPFPEKEMA 326
DB 241 FGELIQPFPEKEMA 254

RESULT 7
US-09-764-868-870
; Sequence 870, Application US/09764868
; Patent No. US20020168711A1

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RESULT 9
US-09-764-868-1179
; Sequence 1179, Application US/09764868
; Patent No. US2002016871A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT32
; CURRENT APPLICATION NUMBER: US/09/764,868
; PRIOR FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1179
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-868-1179

Query Match      22.1%; Score 553; DB 9; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.2e-43;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 RVFFLNVPDSIMERLTIRIDPVGTGERVHMYKPPPTMEIQARLLQNPDKDAEEQVKLM 433
DB 8 RVFFLNVPDSIMERLTIRIDPVGTGERVHMYKPPPTMEIQARLLQNPDKDAEEQVKLM 67

QY 434 DLFYRNSADLEQLYGSATLNGDQDPYTVFYEIESGIINPLPKIP 479
DB 68 DLFYRNSADLEQLYGSATLNGDQDPYTVFYEIESGIINPLPKIP 113

RESULT 10
US-10-141-634-4
; Sequence 4, Application US/10141634
; Publication No. US20030008365A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Xie, Qiongshu
; APPLICANT: Abuin, Alejandro
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0344-USA
; CURRENT APPLICATION NUMBER: US/10/141,634
; PRIOR FILING DATE: 2002-05-08
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 94
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-141-634-4

Query Match      19.6%; Score 491; DB 14; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.8e-37;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 386 MERLTURRIDPVGTGERVHMYKPPPTMEIQARLLQNPDKDAEEQVKLMDFYRNSADLEQ 445
DB 1 MERLTURRIDPVGTGERVHMYKPPPTMEIQARLLQNPDKDAEEQVKLMDFYRNSADLEQ 60

QY 446 LYGSATLNGDQDPYTVFYEIESGIINPLPKIP 479
DB 61 LYGSATLNGDQDPYTVFYEIESGIINPLPKIP 94

RESULT 11
US-10-141-634-4
; Sequence 4, Application US/10141634
; Publication No. US20030008365A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Xie, Qiongshu
; APPLICANT: Abuin, Alejandro
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0344-USA
; CURRENT APPLICATION NUMBER: US/10/141,634
; PRIOR FILING DATE: 2002-05-08
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 94
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-141-634-4

Query Match      19.6%; Score 491; DB 14; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.8e-37;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 386 MERLTURRIDPVGTGERVHMYKPPPTMEIQARLLQNPDKDAEEQVKLMDFYRNSADLEQ 445
DB 1 MERLTURRIDPVGTGERVHMYKPPPTMEIQARLLQNPDKDAEEQVKLMDFYRNSADLEQ 60

QY 446 LYGSATLNGDQDPYTVFYEIESGIINPLPKIP 479
DB 61 LYGSATLNGDQDPYTVFYEIESGIINPLPKIP 94

RESULT 12
US-10-424-599-268668
; Sequence 268668, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 268668
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_8462C.1.pap
US-10-424-599-268668

Query Match      15.1%; Score 378.5; DB 15; Length 307;
Best Local Similarity 35.1%; Pred. No. 2.7e-26;
Matches 88; Conservative 45; Mismatches 89; Indels 29; Gaps 5;

QY 220 LEYHVRVIVPSYKILKVISADQPCVDVFYQALTYVQSNHRTNAPTPRVLLGLGPGVS 279
DB 57 LRHYTH----LPSPTKLKV-----NCSTSEPL--KVMISGAPAS 90

QY 280 GKSLQALLAQRYLNVNCCQLLKAVADRTTFELQPFPEKEMAVPSSLKMKVLSOR 339
DB 91 KGTOCELIVQKFGVLVHISTGDLRLRAEVAAGTEIGNKAKEFMNTGQLVDPDEIVTAMVAAR 150

QY 340 LDQDCIQKQWVLHGVPRDLQARLLNRLGYNPNRVFFLNVPFDSIMERLTIRIDPVGTG 399
DB 151 LAREDEVRRHKGWLLDGYFRSFCQAGSLEKMQIRPDVYVILVDVDEILDRCVGRRLDPVTG 210
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; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 191515
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_14959C.1.pep
; US-10-424-599-191515

Query Match      14.9%; Score 372; DB 15; Length 284;
Best Local Similarity 34.5%; Pred. No. 9.8e-26; Indels 16; Gaps 2;
Matches 79; Conservative 45; Mismatches 89;

QY 265 APPTP-----RVLLGPGVSGKSLQAALLAQKYLNVNVCGLLEKAVAD 309
DB 47 SPFAPNAIHSFSLSVTNEALNVMISGAPASGKTQCHLITNKYGLVHIAAGDILRAEIAI 106
QY 310 RTTFGELIQPFPEKEMAVPDSLLMKVLSQRLDQDCIQKGVHLGVPRDLDOAHLNRLG 369
DB 107 GSDNGKRAKQYMEKGQQLVPDEIVVMVKERLLKPDPSKENGWLLDGPFRSLQATALEALG 166
QY 370 YNPFRVFLNVPDPSIMERLTLRRIDPVTGTERYHLMYKPPPTMEIQARLLQNPDAEQV 429
DB 167 FRPHIFLLLEVEDVLERVVGRLDPVTGKIYHLKYSPPETQETIAARLTQRFDDTEEKV 226
QY 430 KLMKDLFYRNSADLEQLYGS-AITNGDQDPYTVFEYIESGIINPLPK 477
DB 227 KLRNLTHQNVESVLSMYKIDITVKINGNVSKBEVFAQIDSAITSLIEER 275

RESULT 15
US-10-425-114-47870
; Sequence 47870, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 47870
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3060-027-G7_FLI.pep
; US-10-425-114-47870

Query Match      14.5%; Score 363.5; DB 15; Length 303;
Best Local Similarity 37.3%; Pred. No. 6.6e-25; Indels 1; Gaps 1;
Matches 78; Conservative 40; Mismatches 90;

QY 270 RVLLGPGVSGKSLQAALLAQKYLNVNVCGLLEKAVADRTTFGELIQPFPEKEMAVPD 329
DB 88 KVMISGAPASGKTQCELIYKYLQAHISAGDILRAEIAAGSENGKRAKEFMKGQQLVPD 147
QY 330 SLLMKVLSQRLDQDCIQKGVHLGVPRDLDOAHLNRLGYNPNRVFFLNVPDPSIMERL 389
DB 148 EIVVMVKERLRQPDQAOENGWLLDGPFRSYSAQMALETLEIRPDTFTLLDVPDELLVERV 207
QY 390 TLRIDPVTGTERYHLMYKPPPTMEIQARLLQNPDAEQVLEKMDLFYRNSADLEQLYGS 449
DB 208 VGRRLDPVTGKIYHLKYSPPENEHIAASRLTORFDDTEEKVKLRLETTYQNIETSLSTYEN 267

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

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; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
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; LENGTH: 284
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_14959C.1.pep
; US-10-424-599-191515

Query Match      14.9%; Score 372; DB 15; Length 284;
Best Local Similarity 34.5%; Pred. No. 9.8e-26; Indels 16; Gaps 2;
Matches 79; Conservative 45; Mismatches 89;

QY 265 APPTP-----RVLLGPGVSGKSLQAALLAQKYLNVNVCGLLEKAVAD 309
DB 47 SPFAPNAIHSFSLSVTNEALNVMISGAPASGKTQCHLITNKYGLVHIAAGDILRAEIAI 106
QY 310 RTTFGELIQPFPEKEMAVPDSLLMKVLSQRLDQDCIQKGVHLGVPRDLDOAHLNRLG 369
DB 107 GSDNGKRAKQYMEKGQQLVPDEIVVMVKERLLKPDPSKENGWLLDGPFRSLQATALEALG 166
QY 370 YNPFRVFLNVPDPSIMERLTLRRIDPVTGTERYHLMYKPPPTMEIQARLLQNPDAEQV 429
DB 167 FRPHIFLLLEVEDVLERVVGRLDPVTGKIYHLKYSPPETQETIAARLTQRFDDTEEKV 226
QY 430 KLMKDLFYRNSADLEQLYGS-AITNGDQDPYTVFEYIESGIINPLPK 477
DB 227 KLRNLTHQNVESVLSMYKIDITVKINGNVSKBEVFAQIDSAITSLIEER 275

RESULT 15
US-10-425-114-47870
; Sequence 47870, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 47870
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3060-027-G7_FLI.pep
; US-10-425-114-47870

Query Match      14.5%; Score 363.5; DB 15; Length 303;
Best Local Similarity 37.3%; Pred. No. 6.6e-25; Indels 1; Gaps 1;
Matches 78; Conservative 40; Mismatches 90;

QY 270 RVLLGPGVSGKSLQAALLAQKYLNVNVCGLLEKAVADRTTFGELIQPFPEKEMAVPD 329
DB 88 KVMISGAPASGKTQCELIYKYLQAHISAGDILRAEIAAGSENGKRAKEFMKGQQLVPD 147
QY 330 SLLMKVLSQRLDQDCIQKGVHLGVPRDLDOAHLNRLGYNPNRVFFLNVPDPSIMERL 389
DB 148 EIVVMVKERLRQPDQAOENGWLLDGPFRSYSAQMALETLEIRPDTFTLLDVPDELLVERV 207
QY 390 TLRIDPVTGTERYHLMYKPPPTMEIQARLLQNPDAEQVLEKMDLFYRNSADLEQLYGS 449
DB 208 VGRRLDPVTGKIYHLKYSPPENEHIAASRLTORFDDTEEKVKLRLETTYQNIETSLSTYEN 267

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

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Mon Mar 21 09:11:07 2005

us-10-798-773-2.rapb

Page 7

QY 450 AIT-LNGQDPYTVFEYIESGIINPLPKK 477  
Db 268 IIVKQDATVDVFAKIDELGSILEKK 296

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Job time : 153 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 19, 2005, 22:35:46 ; Search time 808 Seconds  
(without alignments)  
10609.705 Million cell updates/sec

Title: US-10-798-773-1  
Perfect score: 1440  
Sequence: 1 atggacccactatcgcccc.....tgcacgaagaatccctctga 1440

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5544816 seqs, 2976611598 residues

Total number of hits satisfying chosen parameters: 11089632

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1440	100.0	1440	14	US-10-141-634-1
2	1440	100.0	1440	19	US-10-798-773-1
3	1440	100.0	1579	17	US-10-094-743-1381
4	1440	100.0	1581	18	US-10-478-146-17
5	1170	81.2	1619	17	US-10-104-047-1657
6	1032.8	71.7	1452	14	US-10-165-800-21
7	1027.6	71.4	1223	9	US-09-764-868-257
8	868	60.3	995	17	US-10-311-034-51
9	761	52.8	1778	13	US-10-098-841-257
10	759.8	52.8	774	14	US-10-165-800-23
11	407	28.3	407	10	US-09-918-995-16667

12	366.6	25.5	447	10	US-09-918-995-29164	Sequence 29164, A
13	322	22.4	509	9	US-09-764-868-255	Sequence 255, App
14	322	22.4	510	9	US-09-764-868-566	Sequence 566, App
15	285	19.8	285	14	US-10-141-634-3	Sequence 3, Appli
16	285	19.8	285	19	US-10-798-773-3	Sequence 3, Appli
17	134.6	9.3	545	16	US-10-029-386-5683	Sequence 5683, Ap
18	132	9.2	132	16	US-10-029-386-19439	Sequence 19439, A
19	92.8	6.4	1496	18	US-10-437-963-18461	Sequence 18461, A
20	88	6.1	23865	18	US-10-719-993-7056	Sequence 7056, Ap
21	87	6.0	1165	18	US-10-435-115-16589	Sequence 16589, A
22	87	6.0	1304	17	US-10-435-114-15576	Sequence 15576, A
23	87	6.0	1489	18	US-10-435-115-16966	Sequence 16966, A
24	87	6.0	2547	18	US-10-767-701-15490	Sequence 15490, A
25	85.4	5.9	1246	17	US-10-425-114-28385	Sequence 28385, A
26	85.4	5.9	1269	17	US-10-425-114-24964	Sequence 24964, A
27	85.4	5.9	1402	18	US-10-425-115-169643	Sequence 169643, A
28	84	5.8	1894	17	US-10-104-047-1583	Sequence 1583, Ap
29	81.4	5.7	1410	17	US-10-424-599-48673	Sequence 48673, A
30	77.6	5.4	654	17	US-10-282-122A-14881	Sequence 14881, A
31	75.8	5.3	1031	17	US-10-424-599-125826	Sequence 125826, A
32	74.4	5.2	663	17	US-10-282-122A-13434	Sequence 13434, A
33	72.6	5.0	1022	18	US-10-767-701-11847	Sequence 11847, A
34	71.6	5.0	813	13	US-10-027-632-10112	Sequence 10112, A
35	71.6	5.0	813	17	US-10-027-632-10112	Sequence 10112, A
36	71	4.9	1028	18	US-10-425-115-145038	Sequence 145038, A
37	69.6	4.8	660	17	US-10-282-122A-12017	Sequence 12017, A
38	69	4.8	642	17	US-10-282-122A-20034	Sequence 20034, A
39	68	4.7	648	9	US-09-815-242-7844	Sequence 7844, Ap
40	68	4.7	648	17	US-10-282-122A-30345	Sequence 30345, A
41	68	4.6	645	9	US-09-815-242-7536	Sequence 7536, Ap
42	66.4	4.6	645	17	US-10-282-122A-13952	Sequence 13952, A
43	63.2	4.4	642	17	US-10-282-122A-23787	Sequence 23787, A
44	63.2	4.4	645	9	US-09-815-242-5978	Sequence 5978, Ap
45	63.2	4.4	645	17	US-10-282-122A-6793	Sequence 6793, Ap

ALIGNMENTS

RESULT 1  
US-10-141-634-1  
; Sequence 1, Application US/10141634  
; Publication No. US20030008365A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Xuanchuan  
; APPLICANT: Xie, Qionghu  
; APPLICANT: Abuin, Alejandro  
; APPLICANT: Walke, D. Wade  
; TITLE OF INVENTION: No. US20030008365A1el Human Kinases and Polynucleotides Encoding  
; FILE REFERENCE: LEX-0344-USA  
; CURRENT APPLICATION NUMBER: US/10/141.634  
; PRIOR FILING DATE: 2002-05-08  
; PRIOR APPLICATION NUMBER: US 60/289,727  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1440  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-141-634-1

Query Match	100.0%	Score 1440;	DB 14;	Length 1440;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1440;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATGGAGCGCCATATCGCCCGCCGATGTCCTCCCGGAGTCCCGAGTGGGGAGGAG	60	
Db	1	ATGGAGCGCCATATCGCCCGCCGATGTCCTCCCGGAGTCCCGAGTGGGGAGGAG	60	
Qy	61	ACCAATCTTCGAGTTGATGAGAAATGCTGGAGCAATCTCTGATCCACGAGCCGAA	120	
Db	61	AACCAATCTTCGAGTTGATGAGAAATGCTGGAGCAATCTCTGATCCACGAGCCGAA	120	

QY	1201	AGGTACCACTCATGTACAGCCACCTCCACCATGAGATCCAGGCTCGCTCTCTGCGAG	1260
DB	1201	AGGTACCACTCATGTACAGCCACCTCCACCATGAGATCCAGGCTCGCTCTCTGCGAG	1260
QY	1261	AACCCAAAGAGTGTCTGAAGAGCAGGTCAAGCTGAAATGACCTGTCTACAGAACTCA	1320
DB	1261	AACCCAAAGAGTGTCTGAAGAGCAGGTCAAGCTGAAATGACCTGTCTACAGAACTCA	1320
QY	1321	GCTGACTTGGAGCAGTGTGTATGGTGGCCATCACTCCATGAGGACACAGGACCCATAC	1380
DB	1321	GCTGACTTGGAGCAGTGTGTATGGTGGCCATCACTCCATGAGGACACAGGACCCATAC	1380
QY	1381	ACAGTCTTCAATACATCGAGTGGGATCAATTAATCCCTGCCCAAGAAAATCCCTCTGA	1440
DB	1381	ACAGTCTTCAATACATCGAGTGGGATCAATTAATCCCTGCCCAAGAAAATCCCTCTGA	1440
RESULT 2			
US-10-798-773-1			
; Sequence 1, Application US/10798773			
; Publication NO. US20050019885A1			
; GENERAL INFORMATION:			
; APPLICANT: Yu, Xuanchuan			
; APPLICANT: Xie, Qionghu			
; APPLICANT: Abuin, Alejandro			
; APPLICANT: Walke, D. Wade			
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same			
; FILE REFERENCE: LEX-0344-USA			
; CURRENT APPLICATION NUMBER: US/10/798,773			
; PRIOR FILING DATE: 2004-03-11			
; PRIOR APPLICATION NUMBER: US/10/141,634			
; PRIOR FILING DATE: 2002-05-08			
; PRIOR APPLICATION NUMBER: US 60/289,727			
; PRIOR FILING DATE: 2001-05-09			
; NUMBER OF SEQ ID NOS: 4			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 1			
; LENGTH: 1440			
; TYPE: DNA			
; ORGANISM: homo sapiens			
US-10-798-773-1			
Query Match 100.0%; Score 1440; DB 19; Length 1440;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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DB	1	ATGAGCGCCACTATCGCCCGCAGCATATCCCGCGAGATGCCCGAGTACCGGGAGGAG	60
QY	61	AACCAATCTTTCGAGTTGATGACAGAACTCTCTGATCCACAGCCCGAA	120
DB	61	AACCAATCTTTCGAGTTGATGACAGAACTCTCTGATCCACAGCCCGAA	120
QY	121	GATCCCATCCCTTATGATCCAGCATTCGATAGAGCAACAGCAATGTGCCAGAT	180
DB	121	GATCCCATCCCTTATGATCCAGCATTCGATAGAGCAACAGCAATGTGCCAGAT	180
QY	181	GTAATATTAGTGTCCACCGCTCAGGGGAAACAACTAGCAATGTGGCTGTGCAAAAT	240
DB	181	GTAATATTAGTGTCCACCGCTCAGGGGAAACAACTAGCAATGTGGCTGTGCAAAAT	240
QY	241	CTGAACAGCAGTCTCTCACCTCGAGAACCTGATCTTAATAGTCTTCTATACGGCC	300
DB	241	CTGAACAGCAGTCTCTCACCTCGAGAACCTGATCTTAATAGTCTTCTATACGGCC	300
QY	301	ACCGAAGCCAGAGGCTTTATCTGAAAGGAGACAGTTCACAGCGCGTGTCTCGTCCAG	360
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QY	361	CTGATTTCAGGAACCGCTGGCTGAAGAGGATTCATCAAGCAGGCGTGGATTCCTGGATGGC	420
DB	361	CTGATTTCAGGAACCGCTGGCTGAAGAGGATTCATCAAGCAGGCGTGGATTCCTGGATGGC	420
QY	121	GATCCCATCCCTTTCATGATCCAGCACTTCATAGAGACAGCAATGTGCCAGGAT	180
DB	121	GATCCCATCCCTTTCATGATCCAGCACTTCATAGAGACAGCAATGTGCCAGGAT	180
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DB	181	GTAATATTAGTGTCCACCGCTCAGGGGAAACAACTAGCAATGTGGCTGTGCAAAAT	240
QY	241	CTGAACAGCAGTCTCTCACCTCGAGAACCTGATCTTAATAGTCTTCTATACGGCC	300
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QY	301	ACCGAAGCCAGAGGCTTTATCTGAAAGGAGACAGTTCACAGCGCGTGTCTCGTCCAG	360
DB	301	ACCGAAGCCAGAGGCTTTATCTGAAAGGAGACAGTTCACAGCGCGTGTCTCGTCCAG	360
QY	361	CTGATTTCAGGAACCGCTGGCTGAAGAGGATTCATCAAGCAGGCGTGGATTCCTGGATGGC	420
DB	361	CTGATTTCAGGAACCGCTGGCTGAAGAGGATTCATCAAGCAGGCGTGGATTCCTGGATGGC	420
QY	421	ATCCCTGAGAGCGGTGAGCAGGCTCTGAGGATCCAGACCTTGGGATCACACCCAGAC	480
DB	421	ATCCCTGAGAGCGGTGAGCAGGCTCTGAGGATCCAGACCTTGGGATCACACCCAGAC	480
QY	481	GTCATTGTGAGTGTCTCCAGACAGGCTCTGATCGAGAGAACTTTGGGAGAGAAATC	540
DB	481	GTCATTGTGAGTGTCTCCAGACAGGCTCTGATCGAGAGAACTTTGGGAGAGAAATC	540
QY	541	GACCCCTCAAACTGGAGAGATTTATCAACACCTTTGATCTGGCCACCGGATCTGAATC	600
DB	541	GACCCCTCAAACTGGAGAGATTTATCAACACCTTTGATCTGGCCACCGGATCTGAATC	600
QY	601	GAGAACCGTCTCATGCTCCAGAGACATCTCAGAGCTGGAGCGGCTCAGAAACTGCTG	660
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QY	661	GAGTATCATAGGAACATGCTCAGGCTCATTCCTCTACCCCAAAATCTCAAAATCATC	720
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QY	721	AGTGTGACAGCAGCTGTGAGCTCTTCTACAGGCTCTGACCTATGTCACCAAGCAAC	780
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QY	781	CATCGTACTAATGCGCGCTTACCCCGAGGCTGTCTGCTCGGCGCTGTGGCAGTGGG	840
DB	781	CATCGTACTAATGCGCGCTTACCCCGAGGCTGTCTGCTCGGCGCTGTGGCAGTGGG	840
QY	841	AAAAGTCTGACGCGCCCTCTCTGCGCCAGAAATACAGGCTTGTCAATGTCTGTGGG	900
DB	841	AAAAGTCTGACGCGCCCTCTCTGCGCCAGAAATACAGGCTTGTCAATGTCTGTGGG	900
QY	901	CAATCTGTGAAGAGCTGTGGCAGATAGACACAGCTTTGGCGAGCTCATCCAGCCCTTC	960
DB	901	CAATCTGTGAAGAGCTGTGGCAGATAGACACAGCTTTGGCGAGCTCATCCAGCCCTTC	960
QY	961	TTTGAAGAGAGATGGCAGTTCCTGACAGCTCTCTCATGAAGTGTGAGCCAGCGCTG	1020
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QY	1021	GACAGCAGAGCTGTGAGAGGCTGGTGTCTACAGGCTCCCGCGGACCTCCGAC	1080
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QY	1141	CAATTTGATTCATGAGAGGCTGTCTCAGAGAGATTCATCAGTCTCACTGGGAA	1200
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Db 541 GACCCCTCAAATCTGAGAGATTTATCACCACCTTTGACTGGCCACCCGATCTGAAATC 600
Qy 601 CAGAACCGTCTCATGGTCCAGAGACATCTCAGAGCTGGAGAGGCTCGAAACTGCTG 660
Db 601 CAGAACCGTCTCATGGTCCAGAGACATCTCAGAGCTGGAGAGGCTCGAAACTGCTG 660
Qy 661 GAGTATCATAGGAACATGCTCAGGGTCAATCCCTCTCTACCCCAAAATCCTCAAAGTCATC 720
Db 661 GAGTATCATAGGAACATGCTCAGGGTCAATCCCTCTCTACCCCAAAATCCTCAAAGTCATC 720
Qy 721 AGTGTGACCGACCATGTGTGACGCTCTTACACGAGCTCTGACTATGTCCAAAGCAAC 780
Db 721 AGTGTGACCGACCATGTGTGACGCTCTTACACGAGCTCTGACTATGTCCAAAGCAAC 780
Qy 781 CATGCTACTAAATGCCCCGTTTACCCGAGGGTGTCTGCTCGGGGCTGTGGCAGTGGG 840
Db 781 CATGCTACTAAATGCCCCGTTTACCCGAGGGTGTCTGCTCGGGGCTGTGGCAGTGGG 840
Qy 841 AAAAGTCTGACGGCCGCTCTGCGCCAGAAATACAGGCTTGTCAATGTCTGTGGG 900
Db 841 AAAAGTCTGACGGCCGCTCTGCGCCAGAAATACAGGCTTGTCAATGTCTGTGGG 900
Qy 901 CAACTGTGAAAGAGGCTGTGGCAGATAGGACCAAGTTTGGCCAGCTCATCCAGCCCTTC 960
Db 901 CAACTGTGAAAGAGGCTGTGGCAGATAGGACCAAGTTTGGCCAGCTCATCCAGCCCTTC 960
Qy 961 TTTGAAAGAGGATGGCAGTTCCTGACAGCCTCTCTCATAGAGTGTCTGAGCCAGGCTG 1020
Db 961 TTTGAAAGAGGATGGCAGTTCCTGACAGCCTCTCTCATAGAGTGTCTGAGCCAGGCTG 1020
Qy 1021 GACACGACGACTGCTATCCAGAAAGCTGGGTGTCTACAGGGCTCTCGGCGGACCTGCAC 1080
Db 1021 GACACGACGACTGCTATCCAGAAAGCTGGGTGTCTACAGGGCTCTCGGCGGACCTGCAC 1080
Qy 1081 CAGGACACCTGCTGAAACCGCTCTGGGCTAATCCCAAGGCTGTCTTCTGAATGTG 1140
Db 1081 CAGGACACCTGCTGAAACCGCTCTGGGCTAATCCCAAGGCTGTCTTCTGAATGTG 1140
Qy 1141 CCATTTGATTCATATGAGCGGCTGACTCTGAGAGAAATGATCCAGTCACTGGGAA 1200
Db 1141 CCATTTGATTCATATGAGCGGCTGACTCTGAGAGAAATGATCCAGTCACTGGGAA 1200
Qy 1201 AGGTACCACTCTATGTACAGCCACTCCACCATGAGATCCAGGCTCGCTCTGCAG 1260
Db 1201 AGGTACCACTCTATGTACAGCCACTCCACCATGAGATCCAGGCTCGCTCTGCAG 1260
Qy 1261 AACCCAAAGATGCTGAAAGCAGTCAAGCTGAAATGGAATGCACTGTCTACAGGAATCA 1320
Db 1261 AACCCAAAGATGCTGAAAGCAGTCAAGCTGAAATGGAATGCACTGTCTACAGGAATCA 1320
Qy 1321 GCTGACTTGGACAGTGTGTATGGGTGGGCAATCACTCAATGGGACCAAGGACCCATAC 1380
Db 1321 GCTGACTTGGACAGTGTGTATGGGTGGGCAATCACTCAATGGGACCAAGGACCCATAC 1380
Qy 1381 ACAGTCTTCGAATACATCAGAGTGGGATCAATTAATCCCTCCCAAGAAATCCCTGTA 1440
Db 1381 ACAGTCTTCGAATACATCAGAGTGGGATCAATTAATCCCTCCCAAGAAATCCCTGTA 1440

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RESULT 3

US-10-094-749-1381

; Sequence 1381, Application US/10094749

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; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOMYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1381
; LENGTH: 1579
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-094-749-1381

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Query Match 100.0%; Score 1440; DB 17; Length 1579;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGAGCGCACTATCGCCCGCCGATATCCCGCCGAGATCCCGCCAGTGGGGAGGAG 60
Db 30 ATGGAGCGCACTATCGCCCGCCGATATCCCGCCGAGATCCCGCCAGTGGGGAGGAG 89
Qy 61 AACCAACATCTTCGAGTGTGATCGAGACATCTGGAGCACTCTGATCCACAGCCCGAA 120
Db 90 AACCAACATCTTCGAGTGTGATCGAGACATCTGGAGCACTCTGATCCACAGCCCGAA 149
Qy 121 GATCCGATCCGCTTCATGATCCAGCACTTGCATAGAGACAAAGCAATGTGCTGCTCAG 180
Db 150 GATCCGATCCGCTTCATGATCCAGCACTTGCATAGAGACAAAGCAATGTGCTGCTCAG 209
Qy 181 GTAATATTAGTGTCCACCGCTCAGGGAAAAACAATAGCAATGTGGCTCTGCAACAT 240
Db 210 GTAATATTAGTGTCCACCGCTCAGGGAAAAACAATAGCAATGTGGCTCTGCAACAT 269
Qy 241 CTGAACACAGCTCTCTCAGCTGAGAGACCTGATCTTAATAGTGTTCCTATAGCGGC 300
Db 270 CTGAACACAGCTCTCTCAGCTGAGAGACCTGATCTTAATAGTGTTCCTATAGCGGC 329
Qy 301 ACCGAAGCCAGAGGCTTTATCTGAAAGAGACAGTTCAGCGGCTGCTGCTGCTCAG 360
Db 330 ACCGAAGCCAGAGGCTTTATCTGAAAGAGACAGTTCAGCGGCTGCTGCTGCTCAG 389
Qy 361 CTGATTCAGGAACGCTTGGCTGAAGAGATTCATCAAGCAGGGCTGGATTCCTGATGGC 420
Db 390 CTGATTCAGGAACGCTTGGCTGAAGAGATTCATCAAGCAGGGCTGGATTCCTGATGGC 449
Qy 421 ATCCCTGAGACGGTGGAGGAGCTCTGAGGATCCAGACCTCTGGGATCACACCCAGAC 480
Db 450 ATCCCTGAGACGGTGGAGGAGCTCTGAGGATCCAGACCTCTGGGATCACACCCAGAC 509
Qy 481 GTCATTGTGCTGAGTGTCTCCAGACAGGCTCTGATCCAGAGAACTTTGGGAGAGAAATC 540

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us-10-798-773-1.rnpb

Mon Mar 21 09:11:06 2005

Db 510 GTCAATGCTGAGTCTCCAGACACGGTCTCTGATCAGAGAAATCTGGGAGAGAAATC 569  
 Qy 541 GACCTCAAACTGAGAGATTTATCACCACCTTTGACTGGCCACCCGAAATCTGAAATC 600  
 Db 570 GACCTCAAACTGAGAGATTTATCACCACCTTTGACTGGCCACCCGAAATCTGAAATC 629  
 Qy 601 CAGAACCGTCTCATGCTGGCCAGAGGACATCTCAGAGCTGGAGACGGCTCAGAAATCTGCTG 660  
 Db 630 CAGAACCGTCTCATGCTGGCCAGAGGACATCTCAGAGCTGGAGACGGCTCAGAAATCTGCTG 689  
 Qy 661 GAGTATCATAGGAACATGCTCAGGCTCATCTCCCTCTACCCCAAAATCTCAAGTCATC 720  
 Db 690 GAGTATCATAGGAACATGCTCAGGCTCATCTCCCTCTACCCCAAAATCTCAAGTCATC 749  
 Qy 721 AGTGTGACACGACATGCTGGAGCTCTTCTACAGGCTCTGACCTATGTCCTCAAGCAAC 780  
 Db 750 AGTGTGACACGACATGCTGGAGCTCTTCTACAGGCTCTGACCTATGTCCTCAAGCAAC 809  
 Qy 781 CATGTAATAATGCCCGCTTCAACCCGAGGCTGCTGCTCGGGCTGTGGCAGTGGG 840  
 Db 810 CATGTAATAATGCCCGCTTCAACCCGAGGCTGCTGCTCGGGCTGTGGCAGTGGG 869  
 Qy 841 AAAAGTCTGAGGCGCCCTCTGCGCCAGAAATACAGGCTTGTCAATGCTGCTGTGGG 900  
 Db 870 AAAAGTCTGAGGCGCCCTCTGCGCCAGAAATACAGGCTTGTCAATGCTGCTGTGGG 929  
 Qy 901 CAACTGCTGAAAGAGGCTGTGGCAGATAGGACAGGTTTGGCAGCTCATCCAGCCCTC 960  
 Db 930 CAACTGCTGAAAGAGGCTGTGGCAGATAGGACAGGTTTGGCAGCTCATCCAGCCCTC 989  
 Qy 961 TTTGAAAGGAGATGGCAGTCTTCTCAGAGCTCTCTCATGAGGTGCTGAGCCAGCGCTG 1020  
 Db 990 TTTGAAAGGAGATGGCAGTCTTCTCAGAGCTCTCTCATGAGGTGCTGAGCCAGCGCTG 1049  
 Qy 1021 GACACGAGGATGTCATCCAGAAAGCTGGGTGTCTACAGCGCTCCCGCGGACCTCGAC 1080  
 Db 1050 GACACGAGGATGTCATCCAGAAAGCTGGGTGTCTACAGCGCTCCCGCGGACCTCGAC 1109  
 Qy 1081 CAGGCAACCTGCTGACCGCTGGGTGTCTACATCCCAAGGCTGTTTCTCAATGTG 1140  
 Db 1110 CAGGCAACCTGCTGACCGCTGGGTGTCTACATCCCAAGGCTGTTTCTCAATGTG 1169  
 Qy 1141 CCAATTTGATTCATCATGAGCGGCTGACTCTGAGAGAAATGATCCAGTCACTGGGAA 1200  
 Db 1170 CCAATTTGATTCATCATGAGCGGCTGACTCTGAGAGAAATGATCCAGTCACTGGGAA 1229  
 Qy 1201 AGGTACACCTCATGTACAGCACTCCACATGAGATCCAGGCTCGCTCTGCGAG 1260  
 Db 1230 AGGTACACCTCATGTACAGCACTCCACATGAGATCCAGGCTCGCTCTGCGAG 1289  
 Qy 1261 AACCAAGGATCTGAAAGAGAGGTCAAGCTGAAATGAGCTGTCTTACAGGAATCA 1320  
 Db 1290 AACCAAGGATCTGAAAGAGAGGTCAAGCTGAAATGAGCTGTCTTACAGGAATCA 1349  
 Qy 1321 GCTGACTTGGAGCAGTTGATGAGGTGGCCATCACCCTCAATGGGGAACAGGACCCATAC 1380  
 Db 1350 GCTGACTTGGAGCAGTTGATGAGGTGGCCATCACCCTCAATGGGGAACAGGACCCATAC 1409  
 Qy 1381 ACAGTCTTCGAATACATCGAGGTGGGATCATTAATCCCTGCGCCCAAGAAATCCCTGGA 1440  
 Db 1410 ACAGTCTTCGAATACATCGAGGTGGGATCATTAATCCCTGCGCCCAAGAAATCCCTGGA 1469

RESULT 4

US-10-478-146-17  
 ; Sequence 17, Application US/10478146  
 ; Publication No. US20040203097A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INCYTE CORPORATION; YUE, Henry;  
 ; APPLICANT: LU, Dying Aina M.; AZIMZAI, Yalda;  
 ; APPLICANT: DING, Li; LEE, Ernestine A.;  
 ; APPLICANT: HAFALIA, April J.A.; BECHA, Shanya D.;

; APPLICANT: TANG, Y. Tom; LAL, Preeti G.;  
 ; APPLICANT: GRIFFIN, Jennifer A.; GURURAJAN, Rajagopal;  
 ; APPLICANT: RAMKUMAR, Javalakmi; ELLIOTT, Vicki S.;  
 ; APPLICANT: ARVIZU, Chandra S.; LUO, Wen;  
 ; APPLICANT: SWARNAKAR, Anita; DUGGAN, Brendan M.;  
 ; APPLICANT: TRAN, Uyen K.; CHAWLA, Narinder K.;  
 ; APPLICANT: GANDHI, Ameena R.; YAO, Monique G.;  
 ; APPLICANT: KHAN, Farrah A.; BAUGHN, Mariah R.;  
 ; APPLICANT: BOROWSKY, Mark L.; ZEBARJADIAN, Yeganeh;  
 ; APPLICANT: RICHARDSON, Thomas W.; MARQUIS, Joseph P.;  
 ; APPLICANT: CHEN, David; JIN, Pei  
 ; TITLE OF INVENTION: KINASES AND PHOSPHATASES  
 ; FILE REFERENCE: PF-0995 USN  
 ; CURRENT APPLICATION NUMBER: US/10/478,146  
 ; CURRENT FILING DATE: 2003-11-18  
 ; PRIOR APPLICATION NUMBER: PCT/US02/16634  
 ; PRIOR FILING DATE: 2002-05-23  
 ; PRIOR APPLICATION NUMBER: US 60/293,665  
 ; PRIOR FILING DATE: 2001-05-24  
 ; PRIOR APPLICATION NUMBER: US 60/298,712  
 ; PRIOR FILING DATE: 2001-06-15  
 ; PRIOR APPLICATION NUMBER: US 60/303,418  
 ; PRIOR FILING DATE: 2001-07-06  
 ; PRIOR APPLICATION NUMBER: US 60/306,967  
 ; PRIOR FILING DATE: 2001-07-19  
 ; PRIOR APPLICATION NUMBER: US 60/308,183  
 ; PRIOR FILING DATE: 2001-07-27  
 ; PRIOR APPLICATION NUMBER: US 60/343,007  
 ; PRIOR FILING DATE: 2001-12-19  
 ; PRIOR APPLICATION NUMBER: US 60/357,675  
 ; PRIOR FILING DATE: 2002-02-15  
 ; PRIOR APPLICATION NUMBER: US 60/376,988  
 ; PRIOR FILING DATE: 2002-04-30  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 17  
 ; LENGTH: 1581  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Incyte ID No: 72063274CB1  
 ; US-10-478-146-17

Query Match 100.0%; Score 1440; DB 18; Length 1581;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ATGGAGCGCCACTATGCGCCCGGACCGCTATCCCGCCGAGATGCCCGAGTACCGGGAGGAG 60  
 Db 15 ATGGAGCGCCACTATGCGCCCGGACCGCTATCCCGCCGAGATGCCCGAGTACCGGGAGGAG 74  
 Qy 61 AACCAATCTTCAGTTGATGACAGACATGCTGGAGCAACTCTGATCCACAGCCCGAA 120  
 Db 75 AACCAATCTTCAGTTGATGACAGACATGCTGGAGCAACTCTGATCCACAGCCCGAA 134  
 Qy 121 GATCCCATCCCTTCATGATCCAGCACTTGCTATAGAGACACGCAATGCGCCAGATT 180  
 Db 135 GATCCCATCCCTTCATGATCCAGCACTTGCTATAGAGACACGCAATGCGCCAGATT 194  
 Qy 181 GTAATATAGTCCACCGCTCAGGGAACAAACAAATGATGCTGGCTCTGCAAAAT 240  
 Db 195 GTAATATAGTCCACCGCTCAGGGAACAAACAAATGATGCTGGCTCTGCAAAAT 254  
 Qy 241 CTGAACAGCAGTCTCTCCACCTCGAGAACCTGATCTTAATGATTTCTTATAGGCC 300  
 Db 255 CTGAACAGCAGTCTCTCCACCTCGAGAACCTGATCTTAATGATTTCTTATAGGCC 314  
 Qy 301 ACCGAGCCAGAGCTTTATCTGCAAGGAGACAGTCTCCAGCGCTGCTCTGCTCCAG 360  
 Db 315 ACCGAGCCAGAGCTTTATCTGCAAGGAGAGACAGTCTCCAGCGCTGCTCTGCTCCAG 374  
 Qy 361 CTGATTTCAGGAACCGCTGCTGGAAGAGGATTCATCAAGCAGGCTGGATCTTGGATGGC 420

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Db 375 CTGATTCAGGACCGCTGGCTGAGAGGATTCATCAGCAGGCTGGATCTCGATGGC 434
Qy 421 ATCCCTGAGACGGCTGAGCAGGCTCTGAGGATTCAGACCTCGGGATCACACCAGACAC 480
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Qy 481 GTCAATGTGCTGAGTGTCTCAGACACCGTCTCTGATCGAGAGAACTTGGGAAACAGATC 540
Db 495 GTCAATGTGCTGAGTGTCTCAGACACCGTCTCTGATCGAGAGAACTTGGGAAACAGATC 554
Qy 541 GACCCCTCAAACTGGAGAGATTTATCACACACCTTTGACTGGCCACCCGATCTGAATC 600
Db 555 GACCCCTCAAACTGGAGAGATTTATCACACACCTTTGACTGGCCACCCGATCTGAATC 614
Qy 601 CAGAACCGTCTCATGTGCGCAGAGGACATCTCAGAGCTGGAGAGCGCTCAGAACTGCTG 660
Db 615 CAGAACCGTCTCATGTGCGCAGAGGACATCTCAGAGCTGGAGAGCGCTCAGAACTGCTG 674
Qy 661 GAGTATCATAGGAACATGCTCAGGGTCATTCCTCTCTACCCCAAAATCCTCAAGTCATC 720
Db 675 GAGTATCATAGGAACATGCTCAGGGTCATTCCTCTCTACCCCAAAATCCTCAAGTCATC 734
Qy 721 AGTGTGACCAAGCCATGTGTGACGCTCTTCTACCAAGGCTCTGACCTATGTCCAAAGCAAC 780
Db 735 AGTGTGACCAAGCCATGTGTGACGCTCTTCTACCAAGGCTCTGACCTATGTCCAAAGCAAC 794
Qy 781 CATCGTACTAATGCCCCGTTTACCCCGAGGGTGTCTGCTGGGCGCTGTGGGCACTGGG 840
Db 795 CATCGTACTAATGCCCCGTTTACCCCGAGGGTGTCTGCTGGGCGCTGTGGGCACTGGG 854
Qy 841 AAAAGTCTGAGGCGCGCTCTGGCCAGAAATACAGGCTGTCAATGTCTGCTGTGGG 900
Db 855 AAAAGTCTGAGGCGCGCTCTGGCCAGAAATACAGGCTGTCAATGTCTGCTGTGGG 914
Qy 901 CAACTGTGAAAGAGGTGTGGCAGATAGGACCAAGTTTGGCAGGCTCTACCCAGCCCTTC 960
Db 915 CAACTGTGAAAGAGGTGTGGCAGATAGGACCAAGTTTGGCAGGCTCTACCCAGCCCTTC 974
Qy 961 TTTGAAAAGGAGATGGCAGTTCCTGACAGCCTCTCTCAAGAGGTGTGAGCCAGCGCTG 1020
Db 975 TTTGAAAAGGAGATGGCAGTTCCTGACAGCCTCTCTCAAGAGGTGTGAGCCAGCGCTG 1034
Qy 1021 GACCAGCAGGACTGCAATCCAGAAAGCTGGGTGTCTACACGGGTTCGGCGGAGCTCGAC 1080
Db 1035 GACCAGCAGGACTGCAATCCAGAAAGCTGGGTGTCTACACGGGTTCGGCGGAGCTCGAC 1094
Qy 1081 CAGGCAACCTGTCTGAACCGCTTGGGCTACAAATCCCAACAGGGTGTCTTCTGAAATGTG 1140
Db 1095 CAGGCAACCTGTCTGAACCGCTTGGGCTACAAATCCCAACAGGGTGTCTTCTGAAATGTG 1154
Qy 1141 CCAATTTGATTCATCATGAGGCGGTGACTCTGAGAGAAATTCATCCAGTCACTGGGAA 1200
Db 1155 CCAATTTGATTCATCATGAGGCGGTGACTCTGAGAGAAATTCATCCAGTCACTGGGAA 1214
Qy 1201 AGGTACCACTCATGTACAGCCACTCCACCATGAGATCCAGGCTGGCTCTGAG 1260
Db 1215 AGGTACCACTCATGTACAGCCACTCCACCATGAGATCCAGGCTGGCTCTGAG 1274
Qy 1261 AACCCAAAGGATGCTGAGAGCAGGTCAAGTGAATGAATGGAATCTGTCTACAGGAATCA 1320
Db 1275 AACCCAAAGGATGCTGAGAGCAGGTCAAGTGAATGAATGGAATCTGTCTACAGGAATCA 1334
Qy 1321 GCTGAATTTGAGCAGTTGTATGGGTCGCGCATCACTCAATGGGAGCAGGACCCATAC 1380
Db 1335 GCTGAATTTGAGCAGTTGTATGGGTCGCGCATCACTCAATGGGAGCAGGACCCATAC 1394
Qy 1381 ACAGTCTTGAATATACATGAGAGTGGGATCAATTAATCCCTCCCAAGAAATCCCTGA 1440
Db 1395 ACAGTCTTGAATATACATGAGAGTGGGATCAATTAATCCCTCCCAAGAAATCCCTGA 1454
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RESULT 5

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US-10-104-047-1657
; Sequence 1657, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20030236392A1el full length cDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1657
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1657
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Query Match 81.2%; Score 1170; DB 17; Length 1619;
Best Local Similarity 93.3%; Pred. No. 0;
Matches 1272; Conservative 0; Mismatches 0; Indels 92; Gaps 1;

Qy 169 GTGCCAGGATTGTAATATTAGTCCACCCGCTCAGGGAAACAAACAATAGCAATGTGG 228
Db 148 GTGCCAGGATTGTAATATTAGTCCACCCGCTCAGGGAAACAAACAATAGCAATGTGG 207
Qy 229 CTCTGCAAAATCTGAAACAGCAGTCTCTCACCCTGGAGAACCTGATCTTAATGAGTTT 288
Db 208 CTCTGCAAAATCTGAAACAGCAGTCTCTCACCCTGGAGAACCTGATCTTAATGAGTTT 267
Qy 289 TCCTATACCGCCACCGAGCCAGAGGCTTTATCTGCAAGAGAGAGTTCCTCCAGCGCG 348
Db 268 TCCTATACCGCCACCGAGCCAGAGGCTTTATCTGCAAGAGAGAGTTCCTCCAGCGCG 327
Qy 349 CTGCTGTCTCAGCTGATTCAGAAACGCTGTGCTGAAAGAGATTCATCAAGCAG----- 402
Db 328 CTGCTGTCTCAGCTGATTCAGAAACGCTGTGCTGAAAGAGATTCATCAAGCAGTTGGA 387
Qy 403 ----- 402
Db 388 GTTCTTGTAAATAGCGGCTTTTCGAGTTTTCATCCGCTAATTCAGTATCTGATGACGTG 447
Qy 403 -----GCTGGATTCGATCGCATCGCATCCTCAGACGCGTG 436
Db 448 GTGGTGACATCTGTATCTGTCTCTCATGGCTGGATTCGGATGGCATCCCTGAGACGCGTG 507
Qy 437 AGCAGGCTCTGAGGATCCAGACCTCTGGGATTCACCCAGACACCTCATTTGCTGAGTG 496
Db 508 AGCAGGCTCTGAGGATCCAGACCTCTGGGATTCACCCAGACACCTCATTTGCTGAGTG 567
Qy 497 CTCAGACACGGTCTGATCGAGAGAACTTGGGAGAGAAATCGACCTCAAACTGGAG 556
Db 568 CTCAGACACGGTCTGATCGAGAGAACTTGGGAGAGAAATCGACCTCAAACTGGAG 627
Qy 557 AGATTATCACACCACTTTGACTGGCCACCCGATCTGAAATCCAGAACCGTCTCATGG 616
Db 628 AGATTATCACACCACTTTGACTGGCCACCCGATCTGAAATCCAGAACCGTCTCATGG 687
Qy 617 TGCCAGAGACATCTCAGAGCTGGAGCGCTCAGAACTCTGGAGTATCATAGGAACA 676
Db 688 TGCCAGAGACATCTCAGAGCTGGAGCGCTCAGAACTCTGGAGTATCATAGGAACA 747
Qy 677 TGCTCAGGGTCATTCCTCTCTACCCCAAAATCCTCAAGTCATCAGTGTGACCGCAT 736
Db 748 TGCTCAGGGTCATTCCTCTCTACCCCAAAATCCTCAAGTCATCAGTGTGACCGCAT 807
Qy 737 GTGTGAGCGTCTTCTACAGGCTCTGACCTATGTCCAAAGCAACCATCTGACTAATGCC 796
Db 808 GTGTGAGCGTCTTCTACAGGCTCTGACCTATGTCCAAAGCAACCATCTGACTAATGCC 867
Qy 797 CGTTCACCCCGAGGCTGCTGCTCGGGCGCTGGGCGAGTGGGAAAGTCTCAGCGCG 856
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QY 781 CATGCTACTAATCCCGCTTCAACCCGAGGGTGTGCTGCTCGGGCTGTGGGCAATGGG 840
Db 783 CATGCTACTAATCCCGCTTCAACCCGAGGGTGTGCTGCTCGGGCTGTGGGCAATGGG 842
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Db 843 AAAAGTCTGAGCGCCGCTCTCTGCCCAGAAATACAGGCTTGTCAATGCTGTGCTGGG 902
QY 901 CAATGCTGAAAGAGGCTGTGCGAGATAGACACAGTTTGGGAGCTCATCCAGCCCTTC 960
Db 903 CAATGCTGAAAGAGGCTGTGCGAGATAGACACAGTTTGGGAGCTCATCCAGCCCTTC 962
QY 961 TTTGAAAGAGGAGTGCAGTTCTCTGACAGCTCTCATGAAGTGTCTGAGCGGCTG 1020
Db 963 TTTGAAAGAGGAGTGC----- 978
QY 1021 GACCAGCAGGACTGCATCCAGAAAGGCTGGGTGCTACACGGGCTCCCGGGACCTCGAC 1080
Db 979 ----- 978
QY 1081 CAGGCACCTGCTGAACCGCTGGGCTACATCCCAACAGGGTGTCTTCTGGAATGTG 1140
Db 979 -----CAGGGTGTCTTCTGGAATGTG 1000
QY 1141 CCATTGATTCCATCATGAGCGGCTGACTCTGAGAGAAATGATCCAGTCACTGGGGAA 1200
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Db 1121 AACCCAAAGAGTGTGAAGAGCAGGTCAAGCTGAAATGGAACCTGTCTACAGGAATCA 1180
QY 1321 GCTGACTTGGAGCAGTGTGTATGGTCCGGCATTACCCCTCAATGGGAGCAGGACCATAC 1380
Db 1181 GCTGACTTGGAGCAGTGTGTATGGTCCGGCATTACCCCTCAATGGGAGCAGGACCATAC 1240
QY 1381 ACAGTCTTCGAATACATCGAGAGTGGGATTAATCCCTGCCCAAGAAATCCCTGGA 1440
Db 1241 ACAGTCTTCGAATACATCGAGAGTGGGATTAATCCCTGCCCAAGAAATCCCTGGA 1300

RESULT 7
US-09-764-868-257
; Sequence 257, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ32
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 257
; LENGTH: 1223
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: SITE
; LOCATION: (78)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (307)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1163)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
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; LOCATION: (1181)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1191)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1193)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1203)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1218)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-764-868-257

Query Match 71.4%; Score 1027.6; DB 9; Length 1223;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1153; Conservative 0; Mismatches 10; Indels 43; Gaps 8;

QY 1 ATGGACCCCACTATCGCCCGCACCGTATCCCCCCCCGAGATGCCAGTACCGGGGAGG 60
Db 6 ATGGACCCCACTATCGCCCGCACCGTATCCCCCCCCGAGA-GCCCCAGTAC-GGGAGGAG 63
QY 61 AACCAACATCTTCGAGTTGATG-----CAG 84
Db 64 AACCAACATCTTCGTTGATGCAAGTATTAAACACCTGGGTGTCTGCCCTGCACCACAG 123
QY 85 AACATGCTGGAGCACTCTCTGATCCACAGCCCGAAGATCCCATCCCTTTCATGATCCAG 144
Db 124 AACATGCTGGAGCACTCTCTGATCCACAGCCCGAAGATCCCATCCCTTTCATGATCCAG 183
QY 145 CATTGTGATAGAGACAACGACAATGTGCCAGGATTGTAAATATTAGTCCACCCGCTCA 204
Db 184 CATTGTGATAGAGACAACGACAATGTGCCAGGATTGTAAATATTAGTCCACCCGCTCA 243
QY 205 GGGAAACAAACATAGCAATGTGCTCTGCAAAACATCTG-AACAGCAGTCTCTCCACGCT 263
Db 244 GGGAAACAAACATAGCAATGTGCTCTGCAAAACATCTGAAACAGAGTCTCTCCACGCT 303
QY 264 GGA-GAACCTGATCTTAATGAGTTTCTTATAGGCGCACCGAGCCAG-AAGGCTTTAT 321
Db 304 GGAAGAACCTGATCTTAATGAGTTTCTTATAGGCGCACCGAGCCAGAAAGGCTTTAT 363
QY 322 CTGCAAGAGAGACAGTTCCACAGCGCTGCTGCTCCAGCTGATTCAGGAACGCTGGCT 381
Db 364 CTGCAAGAGAGACAGTTCCACAGCGCTGCTGCTCCAGCTGATTCAGGAACGCTGGCT 423
QY 382 GAAGAGGATTGCATCAAGCAGGGCTGGATTCTGGATGGCATCCCTGAGAGCGGTGAGCAG 441
Db 424 GAAGAGGATTGCATCAAGCAGGGCTGGATTCTGGATGGCATCCCTGAGAGCGGTGAGCAG 482
QY 442 GCTCTGAGGATCCAGACCCCTGGGGATCACACCCAGACAGCTCATTTGCTGAGTCTCA 501
Db 483 GCTCTGAGGATCCAGACCCCTGGGGATCACACCCAGACAGCTCATTTGCTGAGTCTCA 542
QY 502 GACAGGCTCTGATCGAGAGAACTTGGGGAAGAGAAATGACCCCTCAAACTGGAGAGATT 561
Db 543 GACAGGCTCTGATCGAGAGAACTTGGGGAAGAGAAATGACCCCTCAAACTGGAGAGATT 602
QY 562 TATCACCACTTTTGACTGGGCCACCCGGAATCCAGAACTCCAGAACCTCTCATGTGGCCA 621
Db 603 TATCACCACTTTTGACTGGGCCACCCGGAATCCAGAACTCCAGAACCTCTCATGTGGCCA 662
QY 622 GAGGACATCTCAGAGCTGGAGACGCTCAGAACTCTGGAGTATCATAGGACATCTGTC 681
Db 663 GAGGACATCTCAGAGCTGGAGACGCTCAGAACTCTGGAGTATCATAGGACATCTGTC 722
QY 682 AGGGTCATCTCCCTACCCCAAAATCTCAAGTCTCATGCTGCTGACCGACCATGTGTG 741
Db 723 AGGGTCATCTCCCTACCCCAAAATCTCAAGTCTCATGCTGCTGACCGACCATGTGTG 782
QY 742 GACGTCTTACAGGCTCTGACTTATGTCCAAAGCAACCATCTGTAATGCCCGCTTC 801
```

Db 783 GAGCTCTTACAGGCTCTGACCTATGTCTAAAGCAACATCGTACTAATGCCCGGTC 842  
Qy 802 ACCCGAGGCTGTCTGCTCGGCGCTGTGGGCACTGGGCAAGTCTGAGGCGCGCCCTC 861  
Db 843 ACCCGAGGCTGTCTGCTCGGCGCTGTGGGCACTGGGCAAGTCTGAGGCGCGCCCTC 902  
Qy 862 CTGCCCCAGAAATACAGGCTTGTCAATGTCTGTGTGGGCACTGTGAAAGAGGCTGTG 921  
Db 903 CTGCCCCAGAAATACAGGCTTGTCAATGTCTGTGTGGGCACTGTGAAAGAGGCTGTG 962  
Qy 922 GCAGATAGACCACTTTGGGAGCTCATCAGCCCTTTCTTCAAAAGAGAGTGGCAGTT 981  
Db 963 GCAGATAGACCACTTTGGGAGCTCATCAGCCCTTTCTTCAAAAGAGAGTGGCAGTT 1022  
Qy 982 CTTGACAGCTTCTCATGAAGGCTGTGTGAGCGCGCTGTGACAGGAGTGTGATCCAG 1041  
Db 1023 CTTGACAGCTTCTCATGAAGGCTGTGTGAGCGCGCTGTGACAGGAGTGTGATCCAG 1082  
Qy 1042 AAGGCTGGGTGTACAGCGGCTTCCGCGGAGCTTCCAGCAGCAGCAGCTGTGAAACCGC 1101  
Db 1083 AAGGCTGGGTGTACAGCGGCTTCCGCGGAGCTTCCAGCAGCAGCAGCTGTGAAACCGC 1142  
Qy 1102 CTGGGCTACAA-TCCCAACAGGCTGTGTGTCTTCTGAAATGTGCAATTTGATTCATATGGA 1160  
Db 1143 CTGGGCTACAA-TCCCAACAGGCTGTGTGTCTTCTGAAATGTGCAATTTGATTCATATGGA 1202  
Qy 1161 GCGGCT 1166  
Db 1203 NCGGCT 1208

RESULT 8  
US-10-311-034-51  
; Sequence 51, Application US/10311034  
; Publication No. US20040023242A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: YUE, Henry  
; APPLICANT: LAL, Preeti  
; APPLICANT: BANDMAN, Olga  
; APPLICANT: BOROWSKY, Mark L.  
; APPLICANT: AU-YOUNG, Janice  
; APPLICANT: LU, Yan  
; APPLICANT: GANDHI, Ameena R.  
; APPLICANT: TRIBOULEY, Catherine M.  
; APPLICANT: CHAWLA, Narinder K.  
; APPLICANT: YAO, Monique G.  
; APPLICANT: LU, Dyung Aina M.  
; APPLICANT: GREENWALD, Sara R.  
; APPLICANT: RAMKUMAR, Jayalaxmi  
; APPLICANT: GRIFFIN, Jennifer A.  
; APPLICANT: KEARNEY, Liam  
; APPLICANT: BURFORD, Neil  
; APPLICANT: NGUYEN, Dannel B.  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: HE, Ann  
; APPLICANT: THORNTON, Michael  
; APPLICANT: HAFALIA, April  
; APPLICANT: ARVIZU, Chandra S.  
; APPLICANT: GURURAJAN, Rajagopal  
; APPLICANT: LO, Terence P.  
; APPLICANT: KHAH, Farrah A.  
; APPLICANT: RECIPON, Shirley A.  
; APPLICANT: AZIMZAI, Yalda  
; APPLICANT: POLICKY, Jennifer L.  
; APPLICANT: DING, Li  
; APPLICANT: GREYHER, Megan  
; APPLICANT: ELLIOTT, Vicki S.  
; APPLICANT: THANGAVELU, Kavitha  
; APPLICANT: BATRA, Sajeev  
; APPLICANT: ISON, Craig H.

; TITLE OF INVENTION: HUMAN KINASES  
; FILE REFERENCE: PI-0125 PCT  
; CURRENT APPLICATION NUMBER: US/10/311,034  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;  
; 60/228,056  
; PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-08-25  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PERL Program  
; SEQ ID NO 51  
; LENGTH: 995  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20040023242A1 621293CB1  
; US-10-311-034-51

Query Match 60.3%; Score 868; DB 17; Length 995;

Best Local Similarity 100.0%; Pred. No. 1.5e-269; Indels 0; Gaps 0;  
Matches 868; Conservative 0; Mismatches 0;

Qy 573 CTTTGACTGGCCACCCGAATCTGAAATCCAGAACCGTCTCATGTGTCAGAGGACATCTC 632  
Db 3 CTTTGACTGGCCACCCGAATCTGAAATCCAGAACCGTCTCATGTGTCAGAGGACATCTC 62  
Qy 633 AGAGCTGGAGAGCGCTCAGAACTGCTGGAGTATCATAGGAACATCTCAGGGTCAATTC 692  
Db 63 AGAGCTGGAGAGCGCTCAGAACTGCTGGAGTATCATAGGAACATCTCAGGGTCAATTC 122  
Qy 693 CTCCTACCCCAAAATCCTCAAGTCTCAGTGTGTGACAGCCATGTGTGAGAGCTTCTTA 752  
Db 123 CTCCTACCCCAAAATCCTCAAGTCTCAGTGTGTGACAGCCATGTGTGAGAGCTTCTTA 182  
Qy 753 CCAGGCTCTGACTATGTCCAAAGCAACATCTGTAATGCCCCGTTTACCCCGAGGT 812  
Db 183 CCAGGCTCTGACTATGTCCAAAGCAACATCTGTAATGCCCCGTTTACCCCGAGGT 242  
Qy 813 GCTGCTGCTCGGCGCTGTGGCAGTGGGAAAAGTCTGACAGCGCCCTCTCTGCGCCAGAA 872  
Db 243 GCTGCTGCTCGGCGCTGTGGCAGTGGGAAAAGTCTGACAGCGCGCCCTCTCTGCGCCAGAA 302  
Qy 873 ATACAGGCTTGTCAATGTCTGTGTGGGCACTGCTGAAAGAGGCTGTGGCAGATAGAC 932  
Db 303 ATACAGGCTTGTCAATGTCTGTGTGGGCACTGCTGAAAGAGGCTGTGGCAGATAGAC 362  
Qy 933 CAGCTTTGGCGAGCTCATCCAGCCCTTCTTGAAGAGAGATGGCAGTTCTCTGACAGCT 992  
Db 363 CAGCTTTGGCGAGCTCATCCAGCCCTTCTTGAAGAGAGATGGCAGTTCTCTGACAGCT 422  
Qy 993 CCTCATGAAGGCTGTGAGCCAGCGCTGTGACAGAGGACTGTGATCCAGAAAGGCTGGGT 1052  
Db 423 CCTCATGAAGGCTGTGAGCCAGCGCTGTGACAGAGGACTGTGATCCAGAAAGGCTGGGT 482  
Qy 1053 GCTACAGGCTTCCGCGGAGCTTCCAGCAGGACACCTGCTGAAACCGCTTGGGCTACAA 1112  
Db 483 GCTACAGGCTTCCGCGGAGCTTCCAGCAGGACACCTGCTGAAACCGCTTGGGCTACAA 542  
Qy 1113 TCCCAACAGGCTGTTTTTCTGAAATGTGCCATTTGATTCATGTGAGGCGCTGACTCT 1172  
Db 543 TCCCAACAGGCTGTTTTTCTGAAATGTGCCATTTGATTCATGTGAGGCGCTGACTCT 602  
Qy 1173 GAGAAGATTTGATCCAGTCACTGGGGAAGGTACCACTCATGTGTAAGCCACCTCCAC 1232  
Db 603 GAGAAGATTTGATCCAGTCACTGGGGAAGGTACCACTCATGTGTAAGCCACCTCCAC 662  
Qy 1233 CATGGAGATCCAGGCTCGCCCTCTGTCAGAAACCCAAAGGATGTGTAAGAGGCTCAAGCT 1292  
Db 663 CATGGAGATCCAGGCTCGCCCTCTGTCAGAAACCCAAAGGATGTGTAAGAGGCTCAAGCT 722  
Qy 1293 GAAAATGAGCTGTTCTACAGGAATCAGTGTGAGCAGTGTGATGGGTGCGGCAT 1352





PRIOR FILING DATE: 2000-02-29  
; PRIOR APPLICATION NUMBER: 09/795,038  
; PRIOR FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/186,234  
; PRIOR FILING DATE: 2000-02-29  
; PRIOR APPLICATION NUMBER: 09/781,677  
; PRIOR FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: 60/181,705  
; PRIOR FILING DATE: 2000-02-10  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 774  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-165-800-23

Query Match 52.8%; Score 759.8; DB 14; Length 774;  
Best Local Similarity 99.7%; Pred. No. 1.4e-234;  
Matches 761; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 217 ATAGCAATGTGGCTCTGCAACATCTGAACAGCAGTCTCTCACTCTGGAGAACCTGATC 276  
DB 1 ATGGCAATGTGGCTCTGCAACATCTGAACAGCAGTCTCTCACTCTGGAGAACCTGATC 60  
QY 277 TTAATAGTATTTCTATAGCCGACCGAAGCCGAGAGGCTTTATCTGCAAGGAGACA 336  
DB 61 TTAATAGTATTTCTATAGCCGACCGAAGCCGAGAGGCTTTATCTGCAAGGAGACA 120  
QY 337 GTTCCAGCGCTCTCTGTCAGTCTGATTCAGGAACGCTTGTGTAAGAGGATGATC 396  
DB 121 GTTCCAGCGCTCTCTGTCAGTCTGATTCAGGAACGCTTGTGTAAGAGGATGATC 180  
QY 397 AAGCAGGGCTGATCTGATGAGGATCTCTGAGAGCGTGTGAGAGGATCTGAGATCCAG 456  
DB 181 AAGCAGGGCTGATCTGATGAGGATCTCTGAGAGCGTGTGAGAGGATCTGAGATCCAG 240  
QY 457 ACCCTGGGATCACACCCAGACACCTGATTTGTGCTGAGTGTCCAGACACCGTCTGATC 516  
DB 241 ACCCTGGGATCACACCCAGACACCTGATTTGTGCTGAGTGTCCAGACACCGTCTGATC 300  
QY 517 GAGAGAACTTGGGGAAGAGATCGACCTCAAACTGAGAGATTTATCACACACCTTT 576  
DB 301 GAGAGAACTTGGGGAAGAGATCGACCTCAAACTGAGAGATTTATCACACACCTTT 360  
QY 577 GACTGGCCACCGAATCTGAATCCAGAACCGTCTCATGCTGCCAGAGACATCTCAGAG 636  
DB 361 GACTGGCCACCGAATCTGAATCCAGAACCGTCTCATGCTGCCAGAGACATCTCAGAG 420  
QY 637 CTGGAGACGGCTCAGAACTGTGGAGTATCATAGGAACATCTGAGGGTCAATCCCTCC 696  
DB 421 CTGGAGACGGCTCAGAACTGTGGAGTATCATAGGAACATCTGAGGGTCAATCCCTCC 480  
QY 697 TACCCCAAAATCTCAAGTATCATAGTGTGACCGACCATGTGTGAGCGTCTTTTACCAG 756  
DB 481 TACCCCAAAATCTCAAGTATCATAGTGTGACCGACCATGTGTGAGCGTCTTTTACCAG 540  
QY 757 GCTCTGACCTATGTCCAAAGCAACCATCGTACTAATGCCCGGTTCACCCCGAGGGTGTG 816  
DB 541 GCTCTGACCTATGTCCAAAGCAACCATCGTACTAATGCCCGGTTCACCCCGAGGGTGTG 600  
QY 817 CTGCTGGGCTGTGGGAGTGGGAAAGTCTGCGGCGCCCTCTGCGCCAGAAATAC 876  
DB 601 CTGCTGGGCTGTGGGAGTGGGAAAGTCTGCGGCGCCCTCTGCGCCAGAAATAC 660  
QY 877 AGGCTGTCAATGTCTGCTGGGCAACTGCTGAAAGAGGCTGTGGCAGATAGGACACG 936  
DB 661 AGGCTGTCAATGTCTGCTGGGCAACTGCTGAAAGAGGCTGTGGCAGATAGGACACG 720  
QY 937 TTTGGCAGCTCATCCAGCCCTCTTTGAAAGAGGATGGCAG 979  
DB 721 TTTGGCAGCTCATCCAGCCCTCTTTGAAAGAGGATGGCAG 763

RESULT 11  
US-09-918-995-16667  
; Sequence 16667, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FROM VARIOUS CDNA LIBRARIES  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 16667  
; LENGTH: 407  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-918-995-16667

Query Match 28.3%; Score 407; DB 10; Length 407;  
Best Local Similarity 100.0%; Pred. No. 1.4e-120;  
Matches 407; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 347 CGCTGCTGTCAGCTGATTCAGGAACGCTTGGCTGAAGAGGATTCATCAAGCAGGCT 405  
DB 1 CGCTGCTGTCAGCTGATTCAGGAACGCTTGGCTGAAGAGGATTCATCAAGCAGGCT 60  
QY 407 GGATTCGATGGGATCCCTCGAGACGCTGAGAGGCTCTGAGATCCAGACCTGGGGA 466  
DB 61 GGATTCGATGGGATCCCTCGAGACGCTGAGAGGCTCTGAGATCCAGACCTGGGGA 120  
QY 467 TCACACCCAGACACCTGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 526  
DB 121 TCACACCCAGACACCTGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 180  
QY 527 TGGGGAAGAGATCGAACCTCAAACTGGAGAGATTTATCACACACCTTTGATGGCCAC 586  
DB 181 TGGGGAAGAGATCGAACCTCAAACTGGAGAGATTTATCACACACCTTTGATGGCCAC 240  
QY 587 CCGAATCTGAATCCAGAACCGTCTCATGCTGCCAGAGACATCTCAGAGCTGGAGACGG 646  
DB 241 CCGAATCTGAATCCAGAACCGTCTCATGCTGCCAGAGACATCTCAGAGCTGGAGACGG 300  
QY 647 CTGAGAACTGCTGGAGTATCATAGGAACATCTGAGGATCATTCCTCTACCCCAAAA 706  
DB 301 CTGAGAACTGCTGGAGTATCATAGGAACATCTGAGGATCATTCCTCTACCCCAAAA 360  
QY 707 TCCTCAAAAGTCACTAGTGTGACCGACCATGTGTGGACGCTCTTCTAC 753  
DB 361 TCCTCAAAAGTCACTAGTGTGACCGACCATGTGTGGACGCTCTTCTAC 407

RESULT 12  
US-09-918-995-29164  
; Sequence 29164, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FROM VARIOUS CDNA LIBRARIES  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 29164  
; LENGTH: 447  
; TYPE: DNA



ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(447)  
OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-29164

Query Match 25.5%; Score 366.6; DB 10; Length 447;  
Best Local Similarity 97.6%; Pred. No. 1.7e-107;  
Matches 372; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 1060 GCGGTCCCGCGGACCTCGACAGGACACCTGCTGAACCGCTGGGCTCAATCCCAAC 1119  
Db 51 GCGGTCCCGCGGACCTCGACAGGACACCTGCTGAATGGCTGGTCAATCCCAAC 110  
QY 1120 AGGTGTTTTCTGAATGTGCCATTTGATTCATCATGGAGCGGCTGACTCTGAGAAGA 1179  
Db 111 AGGTGTTTTCTGAATGTGCCATTTGATTCATCATGGAGCGGCTGACTCTGAGAAGA 170  
QY 1180 ATTGATCCAGTCACTGGGGAAGGTACACCTCATGTACAAGCCACCTCCACCATGGAG 1239  
Db 171 ATTGATCCAGTCACTGGGGAAGGTACACCTCATGTACAAGCCACCTCCACCATGGAG 230  
QY 1240 ATCCAGGCTCGCCTCTCGCAAGAACCCAAAGGATGCTGAAGAGAGGTCAAGCTGAAGATG 1299  
Db 231 ATCCAGGCTCGCCTCTCGCAAGAACCCAAAGGATGCTGAAGAGAGGTCAAGCTGAAGATG 290  
QY 1300 GACCTGTTTACAGAACTCAGCTGACTTGGAGCAGTTGTATGGTGGCGCATCACCTC 1359  
Db 291 GACCTGTTTACAGAACTCAGCTGACTTGGAGCAGTTGTATGGTGGCGCATCACCTC 350  
QY 1360 AATGGGACACGAGCCCATACACAGTCTTCGATACATCGAGTGGGATCAATATCC 1419  
Db 351 AATGGGACACGAGCCCATACACAGTCTTCGATACATCGAGTGGGATCAATATCC 410  
QY 1420 CTGCCCAAGAAATCCCTGA 1440  
Db 411 CTGCCCAAGAAATCCCTGA 431

RESULT 13  
US-09-764-868-255  
Sequence 255, Application US/09764868  
Patent No. US20020168711A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PRT32  
CURRENT APPLICATION NUMBER: US/09/764,868  
Prior application data removed - refer to PALM or file wrapper  
NUMBER OF SEQ ID NOS: 1510  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 255  
LENGTH: 509  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-764-868-255

Query Match 22.4%; Score 322; DB 9; Length 509;  
Best Local Similarity 100.0%; Pred. No. 4.8e-93;  
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1119 CAGGGTGTTCCTGAATGTGCCATTTGATTCATCATGGAGCGGCTGACTCTGAGAAG 1178  
Db 58 CAGGGTGTTCCTGAATGTGCCATTTGATTCATCATGGAGCGGCTGACTCTGAGAAG 117  
QY 1179 AATTGATCCAGTCACTGGGGAAGGTACACCTCATGTACAAGCCACCTCCACCATGGA 1238  
Db 118 AATTGATCCAGTCACTGGGGAAGGTACACCTCATGTACAAGCCACCTCCACCATGGA 177  
QY 1239 GATCCAGGCTCGCCTCTCGCAAGAACCCAAAGGATGCTGAAGAGAGGTCAAGCTGAAT 1298

Db 178 GATCAGGCTCGCCTCTCGCAAGAACCCAAAGGATGCTGAAGAGAGGTCAAGCTGAAT 237  
QY 1299 GGCAGCTGTTCTACAGGAACCTCAGCTGACTTGGAGCAGTTGTATCGGTGCGCCATCACCT 1358  
Db 238 GGCAGCTGTTCTACAGGAACCTCAGCTGACTTGGAGCAGTTGTATCGGTGCGCCATCACCT 297  
QY 1359 CAATGGGACAGGACCCATACACAGTCTTCGAATACATCGAGAGTGGGATCAATATCC 1418  
Db 298 CAATGGGACAGGACCCATACACAGTCTTCGAATACATCGAGAGTGGGATCAATATCC 357  
QY 1419 CTGCCCAAGAAATCCCTGA 1440  
Db 358 CTGCCCAAGAAATCCCTGA 379

RESULT 14  
US-09-764-868-566  
Sequence 566, Application US/09764868  
Patent No. US20020168711A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PRT32  
CURRENT APPLICATION NUMBER: US/09/764,868  
Prior application data removed - refer to PALM or file wrapper  
NUMBER OF SEQ ID NOS: 1510  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 566  
LENGTH: 510  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (8)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-764-868-566

Query Match 22.4%; Score 322; DB 9; Length 510;  
Best Local Similarity 100.0%; Pred. No. 4.8e-93;  
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1119 CAGGGTGTTCCTGAATGTGCCATTTGATTCATCATGGAGCGGCTGACTCTGAGAAG 1178  
Db 59 CAGGGTGTTCCTGAATGTGCCATTTGATTCATCATGGAGCGGCTGACTCTGAGAAG 118  
QY 1179 AATTGATCCAGTCACTGGGGAAGGTACACCTCATGTACAAGCCACCTCCACCATGGA 1238  
Db 119 AATTGATCCAGTCACTGGGGAAGGTACACCTCATGTACAAGCCACCTCCACCATGGA 178  
QY 1239 GATCCAGGCTCGCCTCTCGCAAGAACCCAAAGGATGCTGAAGAGTGGGATCAAGCTGAAT 1298  
Db 179 GATCCAGGCTCGCCTCTCGCAAGAACCCAAAGGATGCTGAAGAGTGGGATCAAGCTGAAT 238  
QY 1299 GGCAGCTGTTCTACAGGAACCTCAGCTGACTTGGAGCAGTTGTATGGTGGCGCATCACCT 1358  
Db 239 GGCAGCTGTTCTACAGGAACCTCAGCTGACTTGGAGCAGTTGTATGGTGGCGCATCACCT 298  
QY 1359 CAATGGGACAGGACCCATACACAGTCTTCGAATACATCGAGAGTGGGATCAATATCC 1418  
Db 299 CAATGGGACAGGACCCATACACAGTCTTCGAATACATCGAGAGTGGGATCAATATCC 358  
QY 1419 CTGCCCAAGAAATCCCTGA 1440  
Db 359 CTGCCCAAGAAATCCCTGA 380

RESULT 15  
US-10-141-634-3  
Sequence 3, Application US/10141634  
Publication No. US20030008365A1  
GENERAL INFORMATION:  
APPLICANT: Yu, Xuanchuan

Mon Mar 21 09:11:06 2005

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; APPLICANT: Xie, Qiongsu
; APPLICANT: Abuin, Alejandro
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. US20030008365A1el Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0344-USA
; CURRENT APPLICATION NUMBER: US/10/141,634
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/289,727
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 285
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-141-634-3

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Query Match      19.8; Score 285; DB 14; Length 285;
Best Local Similarity 100.0%; Pred. No. 3.4e-81;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1156 ATGGAGCGGCTGACTCTGAGAGAAATTGATCCAGTCACTGGGGAAGGTACCACTCATG 1215
Db      |||||||
QY 1216 TACAAGCCACCTCCACCATGGAGATCCAGGCTCGCCTCTGAGAACCCCAAGGATGCT 1275
Db      |||||||
QY 61 TACAAGCCACCTCCACCATGGAGATCCAGGCTCGCCTCTGAGAACCCCAAGGATGCT 120
Db      |||||||
QY 1276 GAAGAGCAGGTCAAGCTGAAATGGACCTGTTCTACAGGAACTCAGCTGACTTGGAGCAG 1335
Db      |||||||
QY 121 GAAGAGCAGGTCAAGCTGAAATGGACCTGTTCTACAGGAACTCAGCTGACTTGGAGCAG 180
Db      |||||||
QY 1336 TTGTATGGGTGGGCCATCACCTCAATGGGACAGGACCCATACACAGTCTTCGAATAC 1395
Db      |||||||
QY 181 TTGTATGGGTGGGCCATCACCTCAATGGGACAGGACCCATACACAGTCTTCGAATAC 240
Db      |||||||
QY 1396 ATCGAGAGTGGGATCATTAATCCCTGCCCCAAGAAAATCCCTGA 1440
Db      |||||||
QY 241 ATCGAGAGTGGGATCATTAATCCCTGCCCCAAGAAAATCCCTGA 285
Db      |||||||

```

Search completed: March 20, 2005, 01:40:30  
Job time : 815 secs



QY 361 CTGATTCTAGGAGCGCTGGCTGAAGAGGATTGATCAGAGGGCTGGATTCTGGATGCG 420  
Db 361 CTGATTCTAGGAGCGCTGGCTGAAGAGGATTGATCAGAGGGCTGGATTCTGGATGCG 420  
QY 421 ATCCCTGAGAGCGGTGAGAGGCTCTGAGAGATCAGAGCCCTGGGGATCACACCCAGACAC 480  
Db 421 ATCCCTGAGAGCGGTGAGAGGCTCTGAGAGATCAGAGCCCTGGGGATCACACCCAGACAC 480  
QY 481 GTCAATTGCTGAGTGTCTCAGACACCGTCTGATCGAGAGAACTTTGGGGAGAGAAATC 540  
Db 481 GTCAATTGCTGAGTGTCTCAGACACCGTCTGATCGAGAGAACTTTGGGGAGAGAAATC 540  
QY 541 GACCTCTAAATCGAGAGATTATCACACCACTTTGACTGGCCACCCGAATCTGAAATC 600  
Db 541 GACCTCTAAATCGAGAGATTATCACACCACTTTGACTGGCCACCCGAATCTGAAATC 600  
QY 601 CAGAACGCTCTCATGTTGCCAGAGGACATCTCAGAGCTGGAGACGGCTCAGAAATCTGCTG 660  
Db 601 CAGAACGCTCTCATGTTGCCAGAGGACATCTCAGAGCTGGAGACGGCTCAGAAATCTGCTG 660  
QY 661 GAGTATCATAGAAACATGTCAGGGTCAATCCCTTACCCCAAAATCTCAAGTCATC 720  
Db 661 GAGTATCATAGAAACATGTCAGGGTCAATCCCTTACCCCAAAATCTCAAGTCATC 720  
QY 721 AGTGTGACCAAGCCATGTGGAGCTCTTACAGAGCTCTGACCTATGTCCAAAGCAAC 780  
Db 721 AGTGTGACCAAGCCATGTGGAGCTCTTACAGAGCTCTGACCTATGTCCAAAGCAAC 780  
QY 781 CATCTGACTAATGCCCGCTTACCCCGAGGGTGTCTGCTCGGGCTGTGGGAGTGGG 840  
Db 781 CATCTGACTAATGCCCGCTTACCCCGAGGGTGTCTGCTCGGGCTGTGGGAGTGGG 840  
QY 841 AAAAGTGTGAGGCGCCCTCTCTGCGCCAGAAATACAGGCTGTCAATGTCTGTGGG 900  
Db 841 AAAAGTGTGAGGCGCCCTCTCTGCGCCAGAAATACAGGCTGTCAATGTCTGTGGG 900  
QY 901 CAACTGCTGAAAGAGGCTGTGGCAGATAGGACACAGTTTGGCGAGCTCATCCAGCCCTTC 960  
Db 901 CAACTGCTGAAAGAGGCTGTGGCAGATAGGACACAGTTTGGCGAGCTCATCCAGCCCTTC 960  
QY 961 TTTGAAAGAGATGGAGTCTCTGACAGCTCTCATGAAGTGTCTGAGCAGGCGCTG 1020  
Db 961 TTTGAAAGAGATGGAGTCTCTGACAGCTCTCATGAAGTGTCTGAGCAGGCGCTG 1020  
QY 1021 GACCAAGAGTGTGATCAGAAAGCTGGGTGTCTACAGCGGCTCCCGCGGAGCTCTGAC 1080  
Db 1021 GACCAAGAGTGTGATCAGAAAGCTGGGTGTCTACAGCGGCTCCCGCGGAGCTCTGAC 1080  
QY 1081 CAGGACACCTGCTGAACCGCTGGGCTCAATCCCAACAGGGTGTCTTCTGAACTG 1140  
Db 1081 CAGGACACCTGCTGAACCGCTGGGCTCAATCCCAACAGGGTGTCTTCTGAACTG 1140  
QY 1141 CCAATTGATTCATCATGAGCGGCTGACTCTGAGAGAAATGATCCAGTCACTGGGAA 1200  
Db 1141 CCAATTGATTCATCATGAGCGGCTGACTCTGAGAGAAATGATCCAGTCACTGGGAA 1200  
QY 1201 AGGTACCACTCATGTACAGCCACCTCCACCATGAGATCCAGGCTGCGCTCTGCGAG 1260  
Db 1201 AGGTACCACTCATGTACAGCCACCTCCACCATGAGATCCAGGCTGCGCTCTGCGAG 1260  
QY 1261 AACCCAAAGATGTGAGAGAGGCTCAAGTGAATAATGAACTGTCTACAGGAATCA 1320  
Db 1261 AACCCAAAGATGTGAGAGAGGCTCAAGTGAATAATGAACTGTCTACAGGAATCA 1320  
QY 1321 GCTGACTGAGAGAGTGTGATGCTGGCCATCACCTCAATGGGACAGGACCCATAC 1380  
Db 1321 GCTGACTGAGAGAGTGTGATGCTGGCCATCACCTCAATGGGACAGGACCCATAC 1380  
QY 1381 ACAGTCTTCGAATACATCGAGAGTGGATCATTAATCCCTGCGCCAGAAATCCCTCA 1440  
Db 1381 ACAGTCTTCGAATACATCGAGAGTGGATCATTAATCCCTGCGCCAGAAATCCCTCA 1440

RESULT 2  
US-10-141-634-3  
; Sequence 3, Application US/10141634  
; Patent No. 6734010  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Xuanchuan  
; APPLICANT: Xie, Qiongshu  
; APPLICANT: Abuin, Alejandro  
; APPLICANT: Walke, D. Wade  
; TITLE OF INVENTION: No. 6734010el Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0344-USA  
; CURRENT APPLICATION NUMBER: US/10/141,634  
; CURRENT FILING DATE: 2002-05-08  
; PRIOR APPLICATION NUMBER: US 60/289,727  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 285  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-141-634-3  
Query Match 19.8%; Score 285; DB 4; Length 285;  
Best Local Similarity 100.0%; Pred. No. 9.1e-74;  
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1156 ATGGAGCGGCTGACTCTCAGAGAAATTGATCCAGTCACTGGGAAAGGTACCACTCATG 1215  
Db 1 ATGGAGCGGCTGACTCTCAGAGAAATTGATCCAGTCACTGGGAAAGGTACCACTCATG 60  
QY 1216 TACAGACCACTCCACCACATGAGATCCAGGCTGCGCTCTGCGAGAACCCAAAGGATGCT 1275  
Db 61 TACAGACCACTCCACCACATGAGATCCAGGCTGCGCTCTGCGAGAACCCAAAGGATGCT 120  
QY 1276 GAAGAGCAGCTCAAGCTGAAATGGAACCTGTTCTACAGAACTCAGTGTGAGAGCAG 1335  
Db 121 GAAGAGCAGCTCAAGCTGAAATGGAACCTGTTCTACAGAACTCAGTGTGAGAGCAG 180  
QY 1336 TTGTATGGTGGCCATCACCCTCAATGGGACAGGACCCCATACACAGTCTTCGAATAC 1395  
Db 181 TTGTATGGTGGCCATCACCCTCAATGGGACAGGACCCCATACACAGTCTTCGAATAC 240  
QY 1396 ATCGAGAGTGGATCATTAATCCCTGCGCCCAAGAAATCCCTGA 1440  
Db 241 ATCGAGAGTGGATCATTAATCCCTGCGCCCAAGAAATCCCTGA 285  
RESULT 3  
US-09-513-999C-3495  
; Sequence 3495, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59, US2, REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 3495  
; LENGTH: 264  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 67..264



Qy	987	CAGCCTCCTCATGAAGGTGCTGAGCCAGAGCCCTGGACCAAGAGGACTGTGATTCAGAAAGG	1046
Db	384	CGACATCATCATCGCCCTGATCAAGGAAACGATCAACGAGGCCGATTTGGGCCAAG---GG	440
Qy	1047	CTGGGTGCTACACGGGGTTCCTCCGGGGAACCTCGACACAGGCGACACCTGCTGAACCGCCTGGG	1106
Db	441	CTTCTCTGTTTCGACGGGCTTCCCGCGGACCAATCCCGCAGGCCGGAACGCTGAGAGACGCCCG	500
Qy	1107	CTACAATCCCAACAGAGGTGTTTTTCTCGAATGTGCCATTTTGATTCATCATGAGAGGGCT	1166
Db	501	TGTGAACCATCGAACCACTGCTCGAGATCGCCGTCGACGACGAGAGATCTGTCGCGGTAT	560
Qy	1167	GACTCTGAGAAGAAATTGATCCAGTCACTGGGGAAGGTACCCTCATGCTACAAAGCCACC	1226
Db	561	CGCCGGTCTGTCGGGTGATCCGGCTCCGGCCGGGTGACACACCGAGCGACACCGCC	620

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RESULT 7
US-09-252-991A-4423
; Sequence 4423, Application US/09252991A
; Patent NO. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4423
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4423

```

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; sequence 4526; Application 00/09/252-991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4526
; LENGTH: 849
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-4526

Query Match 4.6%; Score 66.4; DB 4; Length 849;
Best Local Similarity 49.0%; Pred. No. 4.2e-09;
Matches 206; Conservative 0; Mismatches 211; Indels 3; Gaps 1;

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	Query Match	4.6%;	Score 66.4;	DB 4;	Length 849;
	Best Local Similarity	49.0%;	Pred. No. 4.2e-09;		
	Matches 206;	Conservative	0;	Mismatches 211;	Indels 3; Gaps 1;
QY	807	GAGGTTGTCGTCTCGGGCTGTGGCAGTGGGAAAGTCTGCAGGCGCGCCCTCTGGC	866		
DB	204	GGTGTGATTCGTCTCGGGGCACCCGGTCCGCGCAAGCACCAGGACCGTTTCATCAC	263		
QY	867	CCAGAAATACAGGCTTGTCATGTCTGTGTGGCAACTGTGTAAAGAGGTGTGGCAGA	926		
DB	264	CGAGAAGTTCGCAITCCGAGATCTCCACCGGCACATGCTGCGCGCCGAGTCAAGGC	323		
QY	927	TAGGACACGTTTGGGAGCTCATCCAGCCCTCTTTTGAAGAAGAGATGGCAGTTCCTTGA	986		
DB	324	CGGACACCCGCTCGCGACAGAGGTGAAGGCGGTGATGGACAGCGCGGCGCTGGATCCGA	383		

## RESULT 8

US-09-489-039A-5541  
 ; Sequence 5541, Application US/09489039A  
 ; Patent No. 6610836  
 ; GENERAL INFORMATION:

APPLICANT: Gary Breton et. al  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
 FILE REFERENCE: 2709.2004001  
 CURRENT APPLICATION NUMBER: US/09/489.039A  
 CURRENT FILING DATE: 2000-01-27  
 PRIOR APPLICATION NUMBER: US 60/117,747  
 PRIOR FILING DATE: 1999-01-29  
 NUMBER OF SEQ ID NOS: 14342  
 SEQ ID NO 5541  
 LENGTH: 678  
 TYPE: DNA  
 ORGANISM: Klebsiella pneumoniae

US-09-489-039A-5541

Query Match 4.4%; Score 63.2; DB 4; Length 678;  
 Best Local Similarity 48.8%; Pred. No. 3.3e-08;  
 Matches 201; Conservative 0; Mismatches 208; Indels 3; Gaps 1;

QY	815	TGCTCTCGGCGCTGTGGCAGTGGGAAAGTCTGAGGCGCGCTCTGCGCCAGAAAT	874
DB	44	TTCTCTTTGGCGCTCGGCGCGGTTAAGGAATCAGGCTCAGTTTCATATGAGAAAT	103
QY	875	ACAGGCTTGTCAATGCTGTGTGGCAACTCTGAAAGAGCTGTGGCAGATAGGACCA	934
DB	104	ACGTAATTCGCAATCTCCACCGCGATATGTCGCGCGCGGTAAATTCGGCTCTG	163
QY	935	CGTTTGGGAGCTATCCAGCCCTCTTTGAAAGAGATGGCAGTTCCTGACAGCTCC	994
DB	164	AGCTCGGTAAAGCAAGCAAGATATATGACGAGGCAAGCTGGTGACGATGAGCTGG	223
QY	995	TCATGAAGGTGTGAGCCAGCGCTGACACGAGGAGTCTCCAGAGGCTGGGTGC	1054
DB	224	TCATCGCGTGGTGAAGAGGTATCGCCCGAGATTG---CCGTACGCGTCTTCG	280
QY	1055	TACAGCGCTCCCGGAGCTCGACGAGGACACTGCTGAACCGCTGGGCTACAATC	1114
DB	281	TGGACGGTTCGCGGAGCANTCCGAGGCTGAGCCATGAAGAGGCGGCAATACCG	340
QY	1115	CCAACGGGTGTTTTCCTGAATGCAATTTGATCCATCATGGAGCGGCTGACTCTGA	1174
DB	341	TTGATTACGTGCGAATTCGACGTGCGGAGCAACTGATCGTCGACCGCATCGTTGCC	400
QY	1175	GAAGATTGATCCAGTCACTGGGGAAGGTACCACTCATGTACAGGCCACC	1226
DB	401	GTCCGCTCCAGCGGCATCCGCTCGGTATACCAATCAATCAATCGCC	452

RESULT 9

US-08-829-027-2  
 ; Sequence 2, Application US/08829027  
 ; Patent No. 5856160  
 ; GENERAL INFORMATION:  
 APPLICANT: Hillman, Jennifer L.  
 APPLICANT: Shah, Purvi  
 TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/829,027  
 FILING DATE: Herewith  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billings, Lucy J.  
 REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PP-0256 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-855-0555  
 TELEFAX: 415-845-4166  
 TELEX:

INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 854 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: Consensus  
 CLONE: 2122022  
 US-08-829-027-2

Query Match 3.9%; Score 56.8; DB 2; Length 854;  
 Best Local Similarity 48.9%; Pred. No. 2.9e-06;  
 Matches 216; Conservative 0; Mismatches 217; Indels 9; Gaps 2;

QY	805	CCGAGGGTGTGCTGTCTGGGCGCTGTGGGCAAGTCTGAGGAGGCTGTGGCA	864
DB	72	CTGGAGCGGTGATCATGCGGGGCGCGGCTCGGGCAAGGCGCACCGTGTCTGGCGCATC	131
QY	865	GCCAGAAATACAGGCTTGTCAATGTCTGTGGGCAACTGCTGAAAGAGGCTGTGGCA	924
DB	132	ACTACACACTTCGAGCTGAAGCACTCTCCAGCGGGGACTTCTCCGGGACACATGCTG	191
QY	925	GATAGACCACTTTGGGAGCTCATCCAGCCCTCTTTGAAAGGAGATGGCAGTTCTCT	984
DB	192	CGGGGCACAGAAATTTGGCGTGTAGCCAGGCTTTCAITGACCAAGGAAACTCATCCCA	251
QY	985	GACAGCTCTCATGAAGTCTGAGCCGCTCGACGAGGACTGCAATCAGAAA	1044
DB	252	GATGATCATGACTCGGCTG-----GCCCTTCATGAGCTGAAAAAATCTCACCAGTAT	305
QY	1045	GGCTGGTGTCTACAGGCGTCCCGGGAGCTTCGACGAGGACACCTGCTGAACCGCTG	1104
DB	306	AGCTGGCTGTGGATGGTTTTTCCAGGACACTTCCACAGGCAAGAGCCCTAGATAG--A	362
QY	1105	GGCTCAATCCCAACAGGCTGTTTTTCTGAATGTGCCATTTGATTCATCGAGCGG	1164
DB	363	GCTTATCAGATCGACACAGTATTAACTGAAATGTGCCCTTTGAGGTCAITTAACACGC	422
QY	1165	CTGACTCTGAGAAGATTGATCCAGTCACTGGGGAAAGGTACCACTCATGTACAGCCA	1224
DB	423	CTTACTGCTGCTGATTCATCCCGCATGTCGCGGCTCTATAACATTTGAATCAACCT	482
QY	1225	CTCCCAACATGGAGATCCAGG	1246
DB	483	CCAAAACATGTGGGCATTGATG	504

RESULT 10  
 US-09-225-366-2  
 ; Sequence 2, Application US/09225366  
 ; Patent No. 6001624  
 ; GENERAL INFORMATION:  
 APPLICANT: Hillman, Jennifer L.  
 APPLICANT: Shah, Purvi  
 TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/225,366  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/829,027  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0256 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 854 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: Consensus  
CLONE: 2122022  
US-09-225-366-2

Query Match 3.9%; Score 56.8; DB 3; Length 854;  
Best Local Similarity 48.3%; Pred. No. 2,9e-06;  
Matches 216; Conservative 0; Mismatches 217; Indels 9; Gaps 2;

QY 805 CCGAGGCTGCTGCTCGGGCTGTGGGCGATGGGAAAGTCTGCAGGCCCGCCCTCTCG 864  
DB 72 CTGCGCGGTGATCATGTGCGGGCCCGGGCTCGGGCAAGCGCACCGTGTCTGCGGCATC 131  
QY 865 GCCAGAAATACAGGCTGTGATGCTGTGGGCAACTGCTGAAAGAGGCTGTGGCA 924  
DB 132 ACTACACATTCGAGCTGAAGACCTCTCAGCGGGGACCTGCTCCGGGACACATGCTG 191  
QY 925 GATAGGACCACTTTGGCGAGCTCATCCAGCCCTCTTTGAAAAGAGATGGCAGTTCT 984  
DB 192 CGGGGCACAGAAATGGCGTGTAGCCAGGCTTCATTGACCAAGGAAACTCATCCCA 251  
QY 985 GACAGCCTCTCATGAAGTCTGAGCCAGCGCTGAGCAGCAGCAGGACTGCATCCAGAAA 1044  
DB 252 GATGATGTCATGATCGGCTG-----GCCCTTCATGAGCTGAAAATCTCACCCAGTAT 305  
QY 1045 GGCTGGGTGCTACACGGCGTCCCGCGGGAAGCTCGACAGGCACACCTGCTGAACCGCTG 1104  
DB 306 AGCTGGCTGTTGGATGTTTTTCCAAAGACACTTCCACAGCAGAACCCCTAGATAG---A 362  
QY 1105 GGCTACATCCCAACAGGGTGTGTTTCTGATGTCGCAATTTGATTCATCATGGAGCGG 1164  
DB 363 GCTTATCATGATCGACAGTGAATTAACCTGAAATGTCCTTTGAGGTCAATTAACACGC 422  
QY 1165 CTGACTCTGAGAAGAAATGATCCAGTCACTGGGAAAGGATACCACTCATGTATCAAGCCA 1224  
DB 423 CTTACTGCTCGCTGGATTATCCCGCCAGTGGCGAGTCTATTAACATGTAATTAACCCCT 482  
QY 1225 CTTCCCAACCATGGAGATCCAGG 1246  
DB 483 CCCAAACCTGTGGGCAATTGATG 504



EARLIER APPLICATION NUMBER: 60/043,568  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,314  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,569  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,311  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,671  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,674  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,669  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,312  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,313  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,672  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,315  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/056,886  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,877  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,889  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,893  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,630  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,878  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,662  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,872  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,882  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,637  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,903  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,888  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,879  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,880  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,894  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,911  
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EARLIER APPLICATION NUMBER: 60/056,636  
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EARLIER APPLICATION NUMBER: 60/056,874  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,910  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,864  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,631  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,845  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,892  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,761  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/047,595

EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,599  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,588  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,585  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,586  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,590  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,594  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,589  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,593  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,614  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,578  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,576  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/047,501  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,670  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/056,632  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,664  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,876  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,881  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,909  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,875  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,862  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,887  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Query Match 3.9%; Score 56.8; DB 3; Length 1751;  
Best Local Similarity 48.9%; Pred. No. 4,3e-06;  
Matches 216; Conservative 0; Mismatches 217; Indels 9; Gaps 2;

QY 805 CCGAGGCTGCTGCTCGGGCTGTGGGCACTGGGAAAAGTCTGCGAGGCCGCTCTG 864  
Db 116 CTGCGAGCGGTGATCATGTGGGGGCCCCCGGGCTCGGGCAAGGGCACCGTGTGTCGGGCATC 175  
QY 865 GCCCAGAAATACAGGCTTGTCAATGCTGTGGGCAACTGCTGAAAGAGGCTGTGGCA 924  
Db 176 ACTACACACTTCGAGCTGAAGCACCTCTCCAGCGGGACCTGCTCCGGGACCAACATGTC 235  
QY 925 GATAGGACCACTGTTGGCGAGCTCATCCAGGCCCTTCTTTCAGAAAGGAGATGCACTTCT 984  
Db 236 CGGGGCACAGAAATTGGCGTGTAGCCAAAGGCTTTCATTGACCAAGGAACTCATCCCA 295

Mon Mar 21 09:11:06 2005

;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
;; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
;; FILE REFERENCE: CL001307  
;; CURRENT APPLICATION NUMBER: US/09/949,016  
;; CURRENT FILING DATE: 2000-04-14  
;; PRIOR APPLICATION NUMBER: 60/241,755  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/237,768  
;; PRIOR FILING DATE: 2000-10-03  
;; PRIOR APPLICATION NUMBER: 60/231,498  
;; PRIOR FILING DATE: 2000-09-08  
;; NUMBER OF SEQ ID NOS: 207012  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 5838  
;; TYPE: DNA  
;; ORGANISM: Human  
US-09-949-016-5838

Query Match 2.9%; Score 41.8; DB 4; Length 2237;  
Best Local Similarity 44.7%; Pred. No. 0.13; 202; Indels 0; Gaps 0;  
Matches 163; Conservative 0; Mismatches 0; Gaps 0;  
QY 802 ACCCGAGGGTGTCTGCTCGGCGCTGTGGGCGAGTGGGAAAAGTCTGCGAGGCGCCCTC 861  
DB 56 ACCAAGATCATCTTTGTGGTGGGCTGCTCAGGGAAGGCGACCCAGTGTGAGAAG 115  
QY 862 CTGGCCCAAGAAATACAGCTTGTCAATGTCTGTGTGGCACTGCTGAAAAGAGCTGTG 921  
DB 116 ATCGTGCAAGATGTGGTACACCACTCTCCACCGGGGACCTCTCGCGTCCGAGGTC 175  
QY 922 GCAGATAGGACCACTTTGGGCGAGCTCATCCAGGCCCTTTTGAAGAGGAGATGGCAGTT 981  
DB 176 AGCTCAGGCTGGCGAGGGCAAGAGCTGTGGAATCATGGAGAAGGGGCGAGTGT 235  
QY 982 CTGACAGCTCTCATGAAGGTGTGAGCCAGCGCTGGACCGAGGAGTGTGATCCAG 1041  
DB 236 CCACTGGAGACAGTGTGGACATGCTCCGGATGCTGTTGGGCGGATGTTGCGCAAG 295  
QY 1042 AAAGCTGGTGTCTACAGCGCTCCCGGGGACCTTCGACCGAGGACACCTGCTGTAACCGC 1101  
DB 296 AAAGCTTGTGATGATGCTTACCGCGGGAGGTGCGAGGAGAGAGTTTGAGCGA 355  
QY 1102 CTGGGCTACATCCCAACAGGGTGTCTTCTGATGTGCCATTTGATTCATCATGAG 1161  
DB 356 CGGATTGGACAGCCCACTGCTGTGTATGTGGACGCGGCGCTGAGACCATGACCCAG 415  
QY 1162 CGGCT 1166  
DB 416 CGGCT 420

RESULT 14  
US-09-103-840A-2  
; Sequence 2, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103,840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 4403765  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; FEATURE:

QY 985 GACAGCTCTCTCATGAAGTGTGTGAGCCAGCGCTGGACACGAGACTGCAATCCAGAAA 1044  
DB 296 GATGATGTCTATGACTCGGTG-----GCCCTTCATGAGCTGAAAAATCTCACCCAGTAT 349  
QY 1045 GGCTGGGTGTCTACAGCGGTCCCGGGGACCTGCGACGACACCTGCTGAACCGCTG 1104  
DB 350 AGCTGGCTGTGGATGTTTCCAGGACACTTCCACGGCAGAGCCCTAGATAG---A 406  
QY 1105 GGCTACATCCCAACAGGGTGTCTTCTGAATGTGCCATTTGATTCATCATGAGCGG 1164  
DB 407 GCTTATCAGATCCACAGATGATTAACCTGATGTGCCCTTTGAGGTCAATTAACAGCG 466  
QY 1165 CTGACTCTGAGAGAAATGATCCAGTCACTGGGGAAGGTACACCTCATGTACAGCCA 1224  
DB 467 CTTACTGCTGCTGATTCATCCGCGAGTGGCGGAGTCTATAACATTTGAATTTCAACCT 526  
QY 1225 CTTCCACCATGGAGATCCAGG 1246  
DB 527 CCCAAACTGTGGCATGTATG 548

RESULT 12  
US-09-489-039A-3207  
; Sequence 3207, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 3207  
; LENGTH: 1866  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-3207

Query Match 2.9%; Score 41.8; DB 4; Length 1866;  
Best Local Similarity 46.9%; Pred. No. 0.12;  
Matches 130; Conservative 0; Mismatches 147; Indels 0; Gaps 0;  
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DB 1076 TGAAGTGGCGGTGTGCGATGCGCATAGTCAGTACGGCATCTGTGGGAGCTGCGG 1135  
QY 1058 ACGGCTCCCGGGACCTCGACAGGCACTCTGTGAACCGCTGGGCTACATCCCA 1117  
DB 1136 TTGGCGCCCATCTCAGCCAGCATGAGCAGCTGGTGATACCTTGGTGGACAGCTGA 1195  
QY 1118 ACAGGTGTTTTCTGAAATGCCATTTGATTCATCATGAGCGGCTGACTCTGAGAA 1177  
DB 1196 CCAGACCTTGGGCTGGACCGCATCAGGAGAGCAGAGCTGATCGTATGGAAG 1255  
QY 1178 GAATTGATCAGTCACTGGGGAAGGTACCACTCATGTACAGCACTCCACCATGG 1237  
DB 1256 ACGGGCCATATGCGCGCGAGCTGACGACTCCATCGCCAGTGGCTATCTGTATGA 1315  
QY 1238 AGATCCAGGTGCGCTCTGCGAGAACCCAAAGATGC 1274  
DB 1316 AGATGAGGTAGTGTCTGAGATGCAAGGCGACGC 1352

RESULT 13  
US-09-949-016-5838  
; Sequence 5838, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.

OTHER INFORMATION: CDC 1551  
OTHER INFORMATION: "n" bases at various positions throughout the sequence  
OTHER INFORMATION: represent a, t, c or g  
US-09-103-840A-2

Query Match  
Best Local Similarity 2.8%; Score 40.4; DB 3; Length 4403765;  
Matches 110; Conservative 0; Mismatches 116; Indels 0; Gaps 0;  
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DB 828301 GAGAGTTTGTGCTGGGACCGCCCGGGGGGCAAGGGACGCGGGTGAAGCTGGC 828360  
QY 867 CCAGAAATACAGGCTTGTCTATGCTGTGGGCACTGTCTGAAAGAGGCTGTGGCAGA 926  
DB 828361 CGAGAAGCTCCGGATCCCGCAGATCTCCACCGCGCAACTCTTCCGGCGCAACATCGAAGA 828420  
QY 927 TAGGACCAAGTTTGGGAGCTCATCCAGCCCTTCTTTGAAAAGGAGATGGCAGTCTCTGA 986  
DB 828421 GGGCACCAGCTCGGCTGGAAGCAACGCTACTTGGATGCCGTGACTTGGTGGCGTC 828480  
QY 987 CAGCCTCTCATGAAGTGTGAGCCAGCGCTGACCAGCAGGAC 1032  
DB 828481 CGACTTGACCAATGAATCGTTCGACGACCGGCTGAACAATCCGGAC 828526

RESULT 15  
US-09-103-840A-1  
Sequence 1, Application US/09103840A  
Patent No. 6294328  
GENERAL INFORMATION:  
APPLICANT: FLEISCHMAN, Robert D.  
APPLICANT: WHITE, Owen R.  
APPLICANT: FRASER, Claire M.  
APPLICANT: VENTER, John C.  
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
FILE REFERENCE: 24366-20007.00  
CURRENT APPLICATION NUMBER: US/09/103,840A  
CURRENT FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 4411529  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
OTHER INFORMATION: H37Rv  
US-09-103-840A-1

Query Match  
Best Local Similarity 2.8%; Score 40.4; DB 3; Length 4411529;  
Matches 110; Conservative 0; Mismatches 116; Indels 0; Gaps 0;  
QY 807 GAGGGTCTGCTGCTCGGGCTGTGGGCACTGTGGGAAAGTCTGCAGGCGCCCTCTCTGGC 866  
DB 826122 GAGAGTTTGTGCTGGGACCGCCCGGGGGGCAAGGGACGCGGGTGAAGCTGGC 826181  
QY 867 CCAGAAATACAGGCTTGTCTATGCTGTGGGCACTGTCTGAAAGAGGCTGTGGCAGA 926  
DB 826182 CGAGAAGCTCGGGATCCCGCAGATCTCCACCGCGCAACTCTTCCGGCGCAACATCGAAGA 826241  
QY 927 TAGGACCAAGTTTGGGAGCTCATCCAGCCCTTCTTTGAAAAGGAGATGGCAGTCTCTGA 986  
DB 826242 GGGCACCAGCTCGGCTGGAAGCAACGCTACTTGGATGCCGTGACTTGGTGGCGTC 826301  
QY 987 CAGCCTCTCATGAAGTGTGAGCCAGCGCTGACCAGCAGGAC 1032  
DB 826302 CGACTTGACCAATGAATCGTTCGACGACCGGCTGAACAATCCGGAC 826347

Search completed: March 19, 2005, 23:53:51  
Job time : 293 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 19, 2005, 20:29:39 ; Search time 4381 Seconds  
(without alignments)  
12511.424 Million cell updates/sec

Title: US-10-798-773-1

Perfect score: 1440

Sequence: 1 atggcagccactatcgcgc.....tgcccaagaataccctga 1440

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 segs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1.\*

2: gb\_est2.\*

3: gb\_hic.\*

4: gb\_est3.\*

5: gb\_est4.\*

6: gb\_est5.\*

7: gb\_est6.\*

8: gb\_gest1.\*

9: gb\_gest2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1025.4	71.2	2567	3 BC037402	Homo sapi
2	912.8	63.4	1559	3 AK004439	Mus muscu
3	911.8	63.3	1034	5 BM920443	AGENCOURT
4	805.6	55.9	886	6 CD151464	AGENCOURT
5	783.2	54.4	890	4 B1819382	AGENCOURT
6	743.6	51.6	1130	5 BM926674	AGENCOURT
7	723.2	50.2	827	4 B1829572	AGENCOURT
8	703	48.8	710	4 B1767614	AGENCOURT
9	670	46.5	670	4 B1828586	AGENCOURT
10	656	45.6	657	7 CV030269	AGENCOURT
11	591	41.0	721	5 BU617945	AGENCOURT
12	547	38.0	685	5 BQ016312	AGENCOURT
13	518.4	36.0	996	6 BU704667	AGENCOURT
14	514.2	35.7	550	5 BP368808	AGENCOURT
15	513.8	35.7	583	5 BP347783	AGENCOURT
16	463	32.2	463	2 AW069362	AGENCOURT
17	463	32.2	608	5 BU683145	AGENCOURT
18	448	31.1	705	1 A1591934	AGENCOURT
19	441.6	30.7	716	7 CK476676	AGENCOURT
20	432.4	29.3	934	5 BQ942240	AGENCOURT
21	417.6	29.0	794	7 CK594922	AGENCOURT
22	413.8	28.7	857	7 CK653506	AGENCOURT
23	408.6	28.4	789	7 CK470906	AGENCOURT
24	403	28.0	845	7 CK468902	AGENCOURT

25	387.6	26.9	835	7	CK595309	AGENCOURT
26	386.2	26.8	534	1	A1826091	AGENCOURT
27	386	26.8	622	2	BF469787	AGENCOURT
28	383.4	26.6	608	7	CF360290	AGENCOURT
29	377.8	26.2	611	6	CB274665	AGENCOURT
30	362	25.1	838	5	BU938366	AGENCOURT
31	361	25.1	488	5	BM983192	AGENCOURT
32	350.8	24.4	715	7	CM834879	AGENCOURT
33	348.6	24.2	601	7	CO602574	AGENCOURT
34	343	23.8	453	1	A1361512	AGENCOURT
35	341.2	23.7	398	5	BM910115	AGENCOURT
36	323.2	22.4	493	2	AW663881	AGENCOURT
37	322.4	22.4	602	1	AB046366	AGENCOURT
38	322	22.4	436	1	AA580077	AGENCOURT
39	322	22.4	444	1	A1362274	AGENCOURT
40	322	22.4	464	1	A1359456	AGENCOURT
41	322	22.4	500	5	BM100680	AGENCOURT
42	320.4	22.2	552	2	AW974034	AGENCOURT
43	320.4	22.2	850	5	BU954715	AGENCOURT
44	296.6	20.6	730	7	CK653394	AGENCOURT
45	290	20.1	826	5	EX742486	AGENCOURT

## ALIGNMENTS

RESULT 1	BC037402	2567 bp	mrna	linear	HTC 25-MAR-2004
LOCUS	BC037402				
DEFINITION	Homo sapiens chromosome 9 open reading frame 98, mRNA (cDNA clone IMAGE5163904), with apparent retained intron.				
ACCESSION	BC037402				
VERSION	BC037402.1				GI:23336941
KEYWORDS	HTC				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 2567)				
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buotow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stachton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Abramson, P., Frange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helt, E., Kettman, M., Madan, A., Young, A.C., Rodrigues, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y., Skrzyszewski, M.I., Skalska, U., Smal, D.E., Scherch, A., Schein, J.E., Jones, S.O., and Marra, M.A.				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
FORMED	124777932				
REFERENCE	2 (bases 1 to 2567)				
AUTHORS	Strausberg, R.				
TITLE	Direct Submission				
JOURNAL	Submitted (04-SEP-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NIH-MGC Project URL: <a href="http://mgc.ncl.nih.gov">http://mgc.ncl.nih.gov</a>				
COMMENT	Contact: MGC help desk Email: <a href="mailto:cgpps-remail.nih.gov">cgpps-remail.nih.gov</a> Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc.				



Db 2203 AGCTGAAATGACCTGTTCTTACAGGAATCTCAGCTGACTTGGAGCAGTTGTATGGTCTG 2262  
 QY 1348 GCCATCACCTCAATGGGGGACAGACCACATACACAGTCTTCGATACATACGAGTGGG 1407  
 Db 2263 GCCATCACCTCAATGGGGGACAGACCACATACACAGTCTTCGATACATACGAGTGGG 2322  
 QY 1408 ATCAATTAATCCCTCCCAAGAAATCCCTGA 1440  
 Db 2323 ATCAATTAATCCCTCCCAAGAAATCCCTGA 2355

## RESULT 2

AK004439

## LOCUS

DEFINITION Mus musculus 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1190002A17 product:similar to CDNA FLJ32704 FIS, CLONE TEST12000591, WEAKLY SIMILAR TO ADENYLATE KINASE, CHLOROPLAST (EC 2.7.4.3) [Homo sapiens], full insert sequence.  
 AK004439

## ACCESSION

AK004439.1 GI:12835623

## KEYWORDS

HTC; CAP trapper.

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

## PUBLISHED

99279253

## REFERENCE

2

## AUTHORS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 Genome Res. 10 (10), 1617-1630 (2000)

## JOURNAL

20499374

## PUBLISHED

11042159

## REFERENCE

3

## AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, M., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
 Genome Res. 10 (11), 1757-1771 (2000)

## JOURNAL

20530913

## PUBLISHED

11076861

## REFERENCE

4

## AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
 Functional annotation of a full-length mouse cDNA collection  
 Nature 409, 685-690 (2001)

## JOURNAL

409

## PUBLISHED

685-690

## REFERENCE

5

## AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 6 (pages 1 to 1559)  
 Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,

Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tezuka, Y., Toyota, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN) Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

## TITLE

## JOURNAL

## COMMENT

Please visit our web site (http://genome.gsc.riken.jp/) for further details.

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGCGCGCACTCGAGTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGAGCGCGCACTCGAGTCTTTTCTTTTNN 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOUR.

## FEATURES

## source

Location/Qualifiers  
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 /clone="1190002A17"  
 /tissue\_type="whole body"  
 /clone\_lib="RIKEN full-length enriched mouse cDNA library"  
 /dev\_stage="18-day embryo"  
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 /note="putative  
 similar to CDNA FLJ32704 FIS, CLONE TEST12000591, WEAKLY SIMILAR TO ADENYLATE KINASE, CHLOROPLAST (EC 2.7.4.3) (Homo sapiens) (SPT96MA6, evidence: FASTV, 75.5%ID, 99.7%length, match=1433)"  
 1544..1549  
 /note="putative"  
 1559  
 /note="putative"

## misc\_feature

Query Match 63.4%; Score 912.8; DB 3; Length 1559;  
 Best Local Similarity 77.6%; Pred. No. 1.6e-232;  
 Matches 1117; Conservative 0; Mismatches 32; Indels 1; Gaps 1;  
 QY 1 ATGAGCGCCATTCGCGCGCAGCTATCCCGCGAGATGCCCGAGGAGGAG 60  
 Db 29 ATGAGCGCCATTCGCGCGCAGCTATCCCGCGAGATGCCCGAGGAGGAG 60  
 QY 61 AACCAATCTTCGAGTTGATGCAGAACATGCTGGAGCAATCTCTGATCCACGAGCCGAA 120  
 Db 89 TACTACATTTTCGAGATGATGCAGAACATGTTGGAGCAGCTCTGTATCCACGAGGAG 148  
 QY 121 GATCCATCCCTTCATGATCCAGCACTTGTGATAGACACGACATGTCGCGAGT 180  
 Db 149 GACCCATCAGCTTCATGATCACTCACTGCGGAGAACATGATATGTCGAGTGT 208  
 QY 181 GTAATATTAGTCCACCGCCCTCAGGAGAAACACATAGCATGTGCTCTGCAAAAT 240  
 Db 209 GTGATATTAGTCCGCTGCTCAGGAGAAACACATGCGCATGTGCTCTGCAAAAT 268  
 QY 241 CTGACAGCAGTCTCTCCCTCAGGAGAACCTGATCTTAATAGTGTTCCTATAGCGCC 300  
 Db 269 CTAACAGCAACCTCTCATCCCAAGGAGAGCTTACTAGAAAGAGAGTTTCCCGTCTGT 328

301 ACCGAGCCAGAGGCTTTATCTGCAAGGAGAGAGGTTCCAGCGCGTCTGCTCCAG 360  
 329 GTGGAAGCCAGAGTTACTACCAAGGTTTACAGAGAGATCCCAATTCGATTCTTGTCAGT 388  
 361 CTGATTACGAGACGCTGGCTGAAGAGGATGTGATCAAGCAGGCTGGATTCTGATGCGC 420  
 389 CTTGTCCAGGAGGCTCTGAATGAGATGACTGCTCAGAAAGGCTGGATCTGGACGCGC 448  
 421 ATCCCTGAGACGCTGAGCAGGCTCTGAGGATCAGACCCCTGGGATCAGCCAGACAC 480  
 449 ATCCCTGAGAGGCGGAGCAGGCTCTGATGATCAGACCCCTGGGCTGGCCCAAGCAC 508  
 481 GTCAATTGCTGAGTCTCCAGACAGGCTCTGATCAGAGAGAACTTGGGGAAGAGAAATC 540  
 509 GTCAATTGCTGATGCTCCAGACACTGTCTGATGATAGAAATGTGGCAAGCGGATC 568  
 541 GACCTCAAACTGAGAGATTTATFACACACACCTTTGACTGGCCACCCGAAATCTGAATC 600  
 569 GACCTGTCCAGGAGAGATCTATCACACACCTTCGACTGGCCCTCGAGCCTGAATA 628  
 601 CAGAACCGTCTCATGCTGCGAGAGACATCTCAGAGCTGGAGCGCTCAGAAACTGCTG 660  
 629 CAGAACCGCTGAGACGCGGAGGATCTCGAGATCGAAACGCGGCAAGAGCTGCTG 688  
 661 GAGTATCATAGAAACATCGTCAGGCTCAATCCCTCTCTACCCCAAAATCTCAAAGTCATC 720  
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 809 CATGCTACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 868  
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 869 AAGAGACTGACGCTACCTCTCTGCGCCAGAAATATGCGCTGTGAAACATCAGCTGCGGG 928  
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 1081 CAGGCAACCTGCTGAACCGCTGCGGTCTCAATCCCAACAGGCTGTTTTCTGATGCTG 1140  
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 1141 CCAATTTGATTTCAATCAATGAGCGGCTGCTGAGAGAAATTTGATCCAGTCACTGGGAA 1200  
 1169 CCACTGATTTCCATTTCTGGAGCGG- TGACGCTGAGAAAGGACAGCCCTGTCTACAGAGAA 1227  
 1201 AGGTACCACTCATGATACAGGCACTCTCCACCATGAGAGATCCAGGCTCGCTCTCTGCGAG 1260  
 1228 AGGTTCACCTCATGATCAAGAGCCCTCTCCACCATGAGAGTCCAGGCTCGCTCTCTGCGAG 1287  
 1261 AACCCAAAGGATGCTGAAGAGCAGGTCAGCTGAAATGAGCTGTTCTTACAGGACTCA 1320  
 1288 AACCCAAAGGATTCAGAGGAGTGCATCAAGCTCCAAACGAGCTGTTCTTACGAGAACTCT 1347  
 1321 GCTGACTTGGAGGATTTGATGCTGCGGCCATCACCTCTCAATGGGACCAAGACCCCATAC 1380  
 1348 GGGGATCTGGAGGAGTACTAGATCGAGGCATCATTTGTCAACGAGACCAAGGACCTTATAC 1407  
 1381 ACAGTCTTGAATACATCGAGAGTGGATCATTAATCCCTGCGCCAGAAATATCCCTCGA 1440

1408 ACAGTTTTTGTATATAGAGAGCGGATCATTAATCTCTGCGCGAGGAGTTACTCTGA 1467

RESULT 3  
 BM920443 1094 bp mRNA linear EST 12-MAR-2002  
 LOCUS AGENCOURT 6709485 NIH\_MGC\_122 Homo sapiens cDNA clone IMAGE:5750412  
 DEFINITION 5', mRNA sequence.  
 BM920443  
 VERSION BM920443.1 GI:19370822  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1094)  
 NIH-MGC http://mgi.nci.nih.gov/  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: The I.M.A.G.E. Consortium (LLML)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at:  
 http://image.llnl.gov  
 Plate: LLAM12781 row: f column: 13  
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FEATURES  
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 /clone="IMAGE:5750412"  
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 /clone\_lib="NIH MGC 122"  
 /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;  
 Site 1: NotI; Site 2: EcoRV (destroyed); RNA source  
 anonymous pool of 24 week female lung, 16 week female  
 spleen, and 20-22 week male spleens. Library is oligo-dT  
 primed, and directionally cloned (EcoRV site is destroyed  
 upon cloning). Average insert size 1.4 kb, insert size  
 range 1-3 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber  
 (Invitrogen). Research Genetics tracking code 026. Note:  
 this is a NIH\_MGC Library."

ORIGIN  
 Query Match 63.3%; Score 911.8; DB 5; Length 1094;  
 Best Local Similarity 96.0%; Pred. No. 2.7e-232;  
 Matches 1021; Conservative 0; Mismatches 32; Indels 10; Gaps 8;  
 Qy 1 ATGAGCCCACTATGCGCGCGACCTATCCCGCGAGATGCCCGGAGGAGGAG 60  
 Db 26 ATGAGCCCACTATGCGCGCGACCTATCCCGCGAGATGCCCGGAGGAG 85  
 Qy 61 AACCACATCTTCGAGTTGATGTCAGAACATGCTGAGCAACTCTGATCCACGAGCCGAA 120  
 Db 86 AACCACATCTTCGAGTTGATGTCAGAACATGCTGAGCAACTCTGATCCACGAGCCGAA 145  
 Qy 121 GATCCCATCCCTTTCATGATCCAGCACTTCGATAGAGAACACCAATGTGCCAGGATT 180  
 Db 146 GATCCCATCCCTTTCATGATCCAGCACTTCGATAGAGAACACCAATGTGCCAGGATT 205  
 Qy 181 GTAATATTAGTCTCCACCGCTCAGGGGAAACCAATAGCAATGTGGCTCTGCAACAT 240  
 Db 206 GTAATATTAGTCTCCACCGCTCAGGGGAAACCAATAGCAATGTGGCTCTGCAACAT 265  
 Qy 241 CTGAACAGCAGTCTCTCAGCCCTGAGAACCTGATCTTAATGAGTTTCTTATACGGCC 300



Db 266 CTGAACAGCAGTCTCTCCACCCCTGGAGAACCTGATCTTAAATGAGTTTCTTATACGGCC 325  
QY 301 ACCGAGCCAGAGGCTTTTATCTGCAAGGAAGACAGTTCACAGCGCGCTGCTGCTCCAG 360  
Db 326 ACCGAGCCAGAGGCTTTTATCTGCAAGGAAGACAGTTCACAGCGCGCTGCTGCTCCAG 395  
QY 361 CTGATTCAGGAACCGCTGCTGAGAGGATTCATCAAGCAGGGCTGATTCGATGCTGCTGCTG 420  
Db 386 CTGATTCAGGAACCGCTGCTGAGAGGATTCATCAAGCAGGGCTGATTCGATGCTGCTGCTG 445  
QY 421 ATCCCTGAGACCGCTGAGAGGCTTCGAGATTCAGACCTCGGGATCACACCCAGACAC 480  
Db 446 ATCCCTGAGACCGCTGAGAGGCTTCGAGATTCAGACCTCGGGATCACACCCAGACAC 505  
QY 481 GTCAATGCTGAGTGTCTCCAGACACCGCTCTGATCGAGAGAACTTGGGGAAGAGATC 540  
Db 506 GTCAATGCTGAGTGTCTCCAGACACCGCTCTGATCGAGAGAACTTGGGGAAGAGATC 565  
QY 541 GACCCCTCAAACTGGAGAGATTTATCACACCACTTTGACTGCGCCACCGAATCTGAATC 600  
Db 566 GACCCCTCAAACTGGAGAGATTTATCACACCACTTTGACTGCGCCACCGAATCTGAATC 625  
QY 601 CAGAACCGCTCTCATGCTGCCAGAGACATCTCAGAGCTGGAGAGGGCTCAGAACTGCTG 660  
Db 626 CAGAACCGCTCTCATGCTGCCAGAGACATCTCAGAGCTGGAGAGGGCTCAGAACTGCTG 685  
QY 661 GAGTATCATAGAACATGCTCAGAGGTCATTCCTCTTACCCCAAACTCTCAAGTCAATC 720  
Db 686 GAGTATCATAGAACATGCTCAGAGGTCATTCCTCTTACCCCAAACTCTCAAGTCAATC 745  
QY 721 AGTGTGACACGACATGCTGAGAGCTCTTCTACAGGCTCTGACCTATGTCACCAAGCAAC 780  
Db 746 AGTGTGACACGACATGCTGAGAGCTCTTCTACAGGCTCTGACCTATGTCACCAAGCAAC 805  
QY 781 CATCTGACTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 897  
Db 806 CATCTGACTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 865  
QY 840 GAAAGTCTGAGAGCGG - CGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 897  
Db 865 GAAAGTCTGAGAGCGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 865  
QY 898 GGGCAACTGCTGAAAG - AGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 954  
Db 926 GGGGCACTGCTGAAAGAAAGCTGTGGGCAATAGGACCACTTGGGGGAGGTCTATCCG 985  
QY 955 CCCTT - -CTTTGAAAGAGATGGCAGTTCCTG - ACAGCTCTCTCATGAGTGC - TGAG 1010  
Db 986 CCCTTCTCTTTGAAAGAAAGTGGGAGTTCTGTAACAGCTTCTCTGTAAGTGTCTGAC 1045  
QY 1011 CCAGCGCTGAGACGAGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1053  
Db 1046 CAAGCGCTTGGACACGAGCTGGCTCTCCAAAGGCTGGGTG 1088

RESULT 4  
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DEFINITION CD515464 886 bp mRNA linear EST 06-JUN-2003  
AGENCY: 14364661 NIH\_MGC.181 Homo sapiens cDNA clone  
IMAGE:30407307 5', mRNA sequence.

## ACCESSION

CD515464

## VERSION

CD515464.1

## KEYWORDS

EST.

## SOURCE

Homo sapiens

## ORGANISM

Homo sapiens (human)

## REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 886)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH  
Bldg. 31 Rm0A07 Bethesda, MD 20892  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Dr. Michael Brownstein  
cDNA Library Preparation: Invitrogen Corp  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Clone Sequencing by: Agencourt Bioscience Corporation  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: NDAM488 row: h column: 04  
High quality sequence stop: 759.

## FEATURES

## source

1..886

Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:30407307"

/tissue\_type="White Matter"

/dev\_stage="Unknown"

/lab\_host="DH10B-Ton A ( T1 and T5 phage resistances) "

/clone\_lib="NIH\_MGC\_181"

/note="Vector: pCMV-Sport6.1; Site 1: NotI; Site 2: EcoRV

(destroyed); Library is oligo-dT primed and directionally

cloned (EcoRV site is destroyed upon cloning). Average

insert size 1.42 kb. Library was constructed by

(Invitrogen). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match

Best Local Similarity

55.9%; Score 805.6; DB 6; Length 886;

Matches 824; Conservative 0; Mismatches 9; Gaps 1;

QY 1 ATGAGCCGCACTATCCGCGCCGACCGTATCCCGCCGAGATGCCCGAGGAGGAG 60

Db 18 ATGAGCCGCACTATCCGCGCCGACCGTATCCCGCCGAGATGCCCGAGGAGGAG 77

QY 61 AACCAATCTTCCAGTTGATGAGAAATGTCGAGAGCAATCTCTGATCCACGAGCCGAA 120

Db 78 AACCAATCTTCCAGTTGATGAGAAATGTCGAGAGCAATCTCTGATCCACGAGCCGAA 137

QY 121 GATCCATCCCTTCTGATGTCGAGCACTTGCATGAGAGCAATGTCGCGGAGGAT 180

Db 138 GATCCATCCCTTCTGATGTCGAGCACTTGCATGAGAGCAATGTCGCGGAGGAT 197

QY 181 GTAAATATAGTTCCTCCGCGCTCAGGAGAAACCAATAGCAATGTGGCTCTGCAAAAT 240

Db 198 GTAAATATAGTTCCTCCGCGCTCAGGAGAAACCAATAGCAATGTGGCTCTGCAAAAT 257

QY 241 CTGAACAGCAGTCTCTCTCACCCCTGGAGAACTGATCTTAAATGAGTTTCTTATACGCC 300

Db 258 CTGAACAGCAGTCTCTCTCACCCCTGGAGAACTGATCTTAAATGAGTTTCTTATACGCC 317

QY 301 ACCGAGCCAGAGGCTTTATCTGCAAGGAAGACAGTTCACAGCGCGCTGCTGCTCCAG 360

Db 318 ACCGAGCCAGAGGCTTTATCTGCAAGGAAGACAGTTCACAGCGCGCTGCTGCTCCAG 377

QY 361 CTGATTCAGAGACCGCTGCTGAGAGAGATTCATCAAGCAGGGCTGATTCGATGCTG 420

Db 378 CTGATTCAGAGACCGCTGCTGAGAGAGATTCATCAAGCAGGGCTGATTCGATGCTG 437

QY 421 ATCCCTGAGACCGCTGAGAGGCTCTGAGGATTCAGACCTCGGGATCACACCCAGACAC 480

Db 438 ATCCCTGAGACCGCTGAGAGGCTCTGAGGATTCAGACCTCGGGATCACACCCAGACAC 497

QY 481 GTCAATGCTGAGTGTCTCCAGACACCGCTCTGATCGAGAGAACTTGGGGAAGAGATC 540

Db 498 GTCAATGCTGAGTGTCTCCAGACACCGCTCTGATCGAGAGAACTTGGGGAAGAGATC 557

QY 541 GACCTCTCAACTGGAGAGATTTATCAACCACTTTGACTGGCCACCGCAATCTGAAATC 600

Db 558 GACCTCTCAACTGGAGAGATTTATCAACCACTTTGACTGGCCACCGCAATCTGAAATC 617



Email: cgabs-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM1284 row: m column: 11  
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 /note="Organ: pOled lung and spleen; Vector: pCMV-SPORT6;  
 Site 1: NotI; Site 2: EcoRV (destroyed); RNA source  
 anonymous pool of 24 week female lung, 16 week female  
 spleen, and 20-22 week male spleens. Library is oligo-dT  
 primed and directionally cloned (EcoRV site is destroyed  
 upon cloning). Average insert size 1.4 kb, insert size  
 range 1-3 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber  
 (Invitrogen). Research Genetics tracking code 026. Note:  
 this is a NIH\_MGC Library."

# FEATURES

source

## ORIGIN

Query Match 51.6%; Score 743.6; DB 5; Length 1130;  
 Best Local Similarity 92.8%; Pred. No. 2.6e-187;  
 Matches 862; Conservative 0; Mismatches 20; Indels 47; Gaps 6;

QY 1 ATGAGCGGCTATCGCCGACCGGTATCCCGCCGAGATGCCCGATCGCGGAGGAG 60  
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 QY 61 AACCAATCTTCAGTGTGATG-----CAG 84  
 DB 86 AACCAATCTTCAGTGTGATGATGAGGATTAACCACTGGGTGTCTGCCCTGCACCCACAG 145  
 QY 85 AACATGCTGGAGCAATCTCTGATCCACAGCGCCGAGATCCCATCCCTTCATGATCCAG 144  
 DB 146 AACATGCTGGAGCAATCTCTGATCCACAGCGCCGAGATCCCATCCCTTCATGATCCAG 205  
 QY 145 CACTTGATAGAGACACGACATGTCGCCAGGATTTGATATAGTTCAGTCCAGCCGCTCA 204  
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 QY 265 GAGAACCTGATCTTAATCAGTTTTCTTATACGCCACCGAAGAGGCTTTATCTG 324  
 DB 326 GAGAACCTGATCTTAATCAGTTTTCTTATACGCCACCGAAGAGGCTTTATCTG 385  
 QY 325 CAAAGGAAGACAGTCTCCAGCGCTGCTGCTCAGCTGATTCAGGAACGCTGGCTGAA 384  
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 DB 566 ACCTGCTGATCGAGAGAACTTGGGGAAGAGATGACCTCAAACTGGAGAGATTAT 625

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 DB 686 GACATCTCAGAGCTGGAGCGGCTCAGAAAATCTGCTGGAGTATCATAGAACATCGTCAGG 745  
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 QY 802 ACCCCGA---GGGTGCTGCTGCTCGGGCTGTGGG---CAGTGGGAAAAGTCTGACAGGCC 855  
 DB 866 ACCCCGAAGGTTGCTGGCTGCTCGGGCTGTGGGGGGCAAGGGGAAAAGTCTGACAGGCC 925  
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 DB 926 CGCCCTCTCGGGCCCAAAATACAGGTT 954

RESULT 7  
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 ACCESSION BI829572  
 VERSION BI829572.1 GI:15941122  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 827)  
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM11425 row: p column: 02  
 High quality sequence stop: 819.  
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 /organism="Homo sapiens"  
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 directionally cloned (EcoRV site is destroyed upon  
 cloning). Average insert size 1.3 kb, insert size range  
 0.9-3 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber  
 (Invitrogen). Research Genetics tracking code 013. Note:  
 this is a NIH\_MGC Library."

FEATURES  
 source  
 1..827

ORIGIN

Query Match		50.2%; Score 723.2; DB 4; Length 827;
Best Local Similarity		98.8%; Pred. No. 6.7e-182;
Matches 802; Conservative		0; Mismatches 3; Indels 7; Gaps 7;
1		ATGAGCGCCACTATCGCCCC-GACCGTATCCCGCCGAGATGCCCCAGTACGGGGAGA 59
18		ATGAGCGCCACTATCGCGCGCACCGTATCCCGCCGAGATGCCCCAGTACGGGGAGA 77
60		GAACCACTTTCAGTTGATGAGACATGCTGGAGCACTCTCATCCACAGCCGCA 119
78		GAACCACTTTCAGTTGATGAGACATGCTGGAGCACTCTCATCCACAGCCGCA 137
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138		AGATCCCATCCCTTCATGATCCAGCACTTGCATAGAGACACAGCAATGTGCCAGGAT 197
180		TGTAATATTAGTCCACCGCTCAGGGAACACAAATAGCAATGTGGCTGCAACA 239
198		TGTAATATTAGTCCACCGCTCAGGGAACACAAATAGCAATGTGGCTGCAACA 257
240		TCTGAACAGCAGTCTCTCACCCTGGAGAACCTGATCTTAAATGAGTTTCTTATACGGC 299
258		TCTGAACAGCAGTCTCTCACCCTGGAGAACCTGATCTTAAATGAGTTTCTTATACGGC 317
300		CACCGAAGCCAGAGGCTTTATCTGCAAGGAACAGATTCACAGCGCGCTGCTGTCCA 359
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360		GCTGATTCAGAAAGCCTGCTGAGAGGATGATCAACGCGGCTGATTCGGATGG 419
378		GCTGATTCAGAAAGCCTGCTGAGAGGATGATCAACGCGGCTGATTCGGATGG 437
420		CATCCTGAGACGGTGTAGAGGCTCTGAGATCCAGACCTCGGGGATCACACCCAGCA 479
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717		CATCAGTGTGACACGCAATGCT-GGACGCTCTTACAGGCTCTGACCTATGTCCAAA 775
737		CATCAGTGTGACACGCAATGCTGGAGGCTCTTACAGGCTCTGACCTATGTCCAAA 796
776		GCAACCATGTACTAATGCCCGTTTCAACCCG 807
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DEFINITION		mRNA sequence.
ACCESSION		BI767614
VERSION		BI767614.1 GI:15759192
KEYWORDS		EST.
SOURCE		Homo sapiens (human)
ORGANISM		Homo sapiens
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 710)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLNL1527 row: a column: 12  
High quality sequence stop: 710.  
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/lab\_host="DH10B"  
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Site 1: NotI; Site 2: EcoRV (destroyed); RNA source  
anonymous pool of 24 week female lung, 16 week female  
spleen, and 20-22 week male spleens. Library is oligo-dT  
primed, and directionally cloned (EcoRV site is destroyed  
upon cloning). Average insert size 1.4 kb, insert size  
range 1-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 026. Note:  
this is a NIH\_MGC Library."

FEATURES

Source

ORIGIN

Query Match 48.8%; Score 703; DB 4; Length 710;  
Best Local Similarity 100.0%; Pred. No. 1.6e-176;  
Matches 703; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGAGCGCCACTATCGCCCCGACCGTATCCCGCCGAGATGCCCCAGTACGGGGAGGAG 60  
8 ATGAGCGCCACTATCGCCCCGACCGTATCCCGCCGAGATGCCCCAGTACGGGGAGGAG 67  
61 AACCACTCTTCAGTTGATGAGAACATGCTGGAGCAACTCTGATCCACAGCCGAA 120  
68 AACCACTCTTCAGTTGATGAGAACATGCTGGAGCAACTCTGATCCACAGCCGAA 127  
121 GATCCCATCCCTTTCATGATCCAGCACTTGCATAGAGACACGACAATGTGCCAGGATT 180  
128 GATCCCATCCCTTTCATGATCCAGCACTTGCATAGAGACACGACAATGTGCCAGGATT 187  
181 GTAATATTAGTTCACCGCTCAGGAAACAAATAAGCAATGTGGCTCTGCAAAACAT 240  
188 GTAATATTAGTTCACCGCTCAGGAAACAAATAAGCAATGTGGCTCTGCAAAACAT 247  
241 CTGAACAGCAGTCTCTCTCACCTGGAGAACCTGATCTTAAATGAGTTTCTTATAGGCC 300  
248 CTGAACAGCAGTCTCTCTCACCTGGAGAACCTGATCTTAAATGAGTTTCTTATAGGCC 307  
301 ACCGAGCCAGAGGCTTTATCTGCAAGGAGACAGTTCCACAGCGCTGCTCTCCAG 360  
308 ACCGAGCCAGAGGCTTTATCTGCAAGGAGACAGTTCCACAGCGCTGCTCTCCAG 367  
361 CTGATTCAGAAACCGCTGGCTGAAGAGGATTGATCAAGCAGGGCTGGATTCTGGATGGC 420  
368 CTGATTCAGAAACCGCTGGCTGAAGAGGATTGATCAAGCAGGGCTGGATTCTGGATGGC 427  
421 ATCCCTCAGACGGCTGAGCAGGCTCTGAGGATCCAGACCTGGGATCCACCCAGCAC 480  
428 ATCCCTCAGACGGCTGAGCAGGCTCTGAGGATCCAGACCTGGGATCCACCCAGCAC 487  
481 GTCAATGTGTGAGTGTCTCCAGACACGCTCTGATCCAGAGAACTTTGGGGAAGAGATC 540

Db 488 GTCAATGTCGTGAGTCTCCAGACACCGTCTCTGATCGAGAGAACTTGGGGAAGAATC 547  
 QY 541 GACCTCAATCGGAGAGATTATCACACACCTTTGACTGGCCACCCGAAATCTGAATC 600  
 Db 548 GACCTCAATCGGAGAGATTATCACACACCTTTGACTGGCCACCCGAAATCTGAATC 607  
 QY 601 CAGAACCGTCTCATGTCGACAGAGACATCTCAGAGCGGCTCAGAACTCTG 660  
 Db 608 CAGAACCGTCTCATGTCGACAGAGACATCTCAGAGCGGCTCAGAACTCTG 667  
 QY 661 GACTATCATAGGAACATCGTCAGGCTCATTCCTCTACCCCA 703  
 Db 668 GACTATCATAGGAACATCGTCAGGCTCATTCCTCTACCCCA 710

RESULT 9  
 BI828586  
 LOCUS  
 DEFINITION 670 bp mRNA linear EST 04-OCT-2001  
 603078486F1 NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:5170317 5',  
 mRNA sequence.  
 BI828586  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: L1AM1423 row: k column: 22  
 High quality sequence stop: 670.

FEATURES  
 source  
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 location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
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 /clone="IMAGE:5170317"  
 /tissue\_type="medulla"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH MGC 119"  
 /note="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI;  
 Site 2: EcoRV (destroyed); RNA source normal medulla from  
 anonymous male age 27. Library is oligo-dT primed and  
 directionally cloned (EcoRV site is destroyed upon  
 cloning). Average insert size 1.3 kb, insert size range  
 0.9-3 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber  
 (Invitrogen). Research Genetics tracking code 013. Note:  
 this is a NIH\_MGC Library."

ORIGIN  
 Query Match 46.5%; Score 670; DB 4; Length 670;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-167;  
 Matches 670; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 34 CCGAGATCCCCAGTACGGGAGAGAACACATCTTCGATTGATCGAGACATCGT 93  
 Db 1 CCGAGATCCCCAGTACGGGAGAGAACACATCTTCGATTGATCGAGACATCGT 60  
 QY 94 GAGCAATCTCTGATCCACGACCGGAGATCCCATCCCTTCATGATCCGACCTTGCAT 153  
 Db 61 GAGCAATCTCTGATCCACGACCGGAGATCCCATCCCTTCATGATCCGACCTTGCAT 120

QY 154 AGAGACAACGACAAATGTGGCCAGGATTGTAATATTAGTTCACCGGCTCAGGAGAAAAACA 213  
 Db 121 AGAGACAACGACAAATGTGGCCAGGATTGTAATATTAGTTCACCGGCTCAGGAGAAAAACA 180  
 QY 214 ACAATAGCAATGTGGCTCTGCAAAACATCTGAAACACAGCTTCCTCACCCCTGGAGAACCTG 273  
 Db 181 ACAATAGCAATGTGGCTCTGCAAAACATCTGAAACACAGCTTCCTCACCCCTGGAGAACCTG 240  
 QY 274 ATCTTAATAGTATTTTCTTATACGGCCACCGAAGCCAGAGGCTTTATCTGCAAGGAAG 333  
 Db 241 ATCTTAATAGTATTTTCTTATACGGCCACCGAAGCCAGAGGCTTTATCTGCAAGGAAG 300  
 QY 334 ACAGTTCGCCAGCGGCTGCTGCTCAGCTGATTCAGGAACCGCTGGCTGAAGAGGATTGC 393  
 Db 301 ACAGTTCGCCAGCGGCTGCTGCTCAGCTGATTCAGGAACCGCTGGCTGAAGAGGATTGC 360  
 QY 394 ATCAAGCAGGGCTGGATTCTGGATGGCATCCCTCAGACGGCTGAGCAGGCTCTGAGGATC 453  
 Db 361 ATCAAGCAGGGCTGGATTCTGGATGGCATCCCTCAGACGGCTGAGCAGGCTCTGAGGATC 420  
 QY 454 CAGACCTCTGGGGATCACACCAGACACCTCATCTGCTGAGTGTCTCCAGACACGGTCTG 513  
 Db 421 CAGACCTCTGGGGATCACACCAGACACCTCATCTGCTGAGTGTCTCCAGACACGGTCTG 480  
 QY 514 ATCCAGAGAACTTTGGGAGAGAGATCGACCTCAAACTGAGAGATTTATCACACACC 573  
 Db 481 ATCCAGAGAACTTTGGGAGAGAGATCGACCTCAAACTGAGAGATTTATCACACACC 540  
 QY 574 TTGACTGGCCACCCGAAATCTGAAATCCAGAACCGTCTCATGTGTCAGAGACATCTCA 633  
 Db 541 TTGACTGGCCACCCGAAATCTGAAATCCAGAACCGTCTCATGTGTCAGAGACATCTCA 600  
 QY 634 GAGCTGAGACCGGCTCAGAACTCTGGAGTATCATAGGAACATCTCAGGCTCATTTCCC 693  
 Db 601 GAGCTGAGACCGGCTCAGAACTCTGGAGTATCATAGGAACATCTCAGGCTCATTTCCC 660  
 QY 694 TCCTACCCCA 703  
 Db 661 TCCTACCCCA 670

RESULT 10  
 CV030269  
 LOCUS  
 DEFINITION 9331 Full Length cDNA from the Mammalian Gene Collection Homo  
 sapiens cDNA 5' similar to BC034776, mRNA sequence.  
 CV030269  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 657)  
 Rual, J.F., Hirozane-Kishikawa, T., Hao, T., Bertin, N., Li, S.,  
 Driect, A., Li, N., Rosenberg, J., Lamesch, P., Vidalain, P.O.,  
 Clingingsmith, T.R., Hartley, J.L., Esposito, D., Cheo, D., Moore, T.,  
 Simmons, B., Sequerra, R., Bosak, S., Doucette-Stamm, L., Le Peuch, C.,  
 Vandenhaute, J., Cusick, M.E., Albala, J.S., Hill, D.E. and Vidal, M.  
 Human ORFome Version 1.1: a Platform for Reverse Proteomics  
 Genome Res. (2004) In press  
 Contact: Vidal M  
 Marc Vidal Laboratory  
 Dana Farber Cancer Institute  
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA  
 Tel: 617 632 5180  
 Fax: 617 632 5739  
 Email: Marc.Vidale@dfci.harvard.edu  
 ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF  
 results from a PCR reaction using an MGC full-length cDNA as  
 template DNA and ORF specific primers  
 PCR Primers

FORWARD: ATGAGCCCACTATCGCC  
BACKWARD: CAGGGATTTCTTGGCAGG  
Insert Length: 657 Std Error: 60.00  
Plate: 11065 row: 11 column: E  
Seq primer: ACTGGCGTGGTTTACACAGCTGCTGACTGGGAAC  
High quality sequence start: 97  
High quality sequence stop: 656  
POLYA=No.

FEATURES  
source  
1. .657  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="mixed"  
/clone\_lib="Full Length cDNA from the Mammalian Gene Collection"  
/note="Vector: mixed; The ORFs were PCR amplified from the MGC (Mammalian Gene Collection) as of April 2004 and cloned by recombinational Gateway cloning into pDONR223 Donor vector. Reference : MGC (Mammalian Gene Collection) Program Team, Generation and Initial Analysis of more than 15,000 Full-length Human and Mouse cDNA Sequences. PNAS, 2002, 99(26), 16899-16903"

ORIGIN  
Query Match 45.6%; Score 656; DB 7; Length 657;  
Best Local Similarity 99.8%; Pred. No. 5.8e-164;  
Matches 656; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGCCCACTATCGCCCGACGGTATCCCCCGAGATGCCCGAGTACGGGGAGGAG 60  
DB 1 ATGAGCCCACTATCGCCCGACGGTATCCCCCGAGATGCCCGAGTACGGGGAGGAG 60  
QY 61 AACCATCTTCGAGTTCATCAGAACATCTGTGAGCAACTCTGTATCCACCCCGAA 120  
DB 61 AACCATCTTCGAGTTCATCAGAACATCTGTGAGCAACTCTGTATCCACCCCGAA 120  
QY 121 GATCCATCCCTTCATGATCAGACATCTGTATGAGAACAGCAATGTGCCAGATT 180  
DB 121 GATCCATCCCTTCATGATCAGACATCTGTATGAGAACAGCAATGTGCCAGATT 180  
QY 181 GTAATATTAGTTCACCGCCCTCAGGAAACAAATAGCAATGTGCTCTGCAACAT 240  
DB 181 GTAATATTAGTTCACCGCCCTCAGGAAACAAATAGCAATGTGCTCTGCAACAT 240  
QY 241 CTGAACAGAGTCTCTCACCCTGAGAACCTGATCTTAATGATTTCTTATACGGCC 300  
DB 241 CTGAACAGAGTCTCTCACCCTGAGAACCTGATCTTAATGATTTCTTATACGGCC 300  
QY 301 ACCGAAGCCAGAGGCTTTATCTGCAAGGAAGACATGTCAGCGCGCTGCTGCCAG 360  
DB 301 ACCGAAGCCAGAGGCTTTATCTGCAAGGAAGACATGTCAGCGCGCTGCTGCCAG 360  
QY 361 CTGATTCAGAACGCTGCTGAGAGGATTCATCAAGCAGGCTGGATTCTGGATGCG 420  
DB 361 CTGATTCAGAACGCTGCTGAGAGGATTCATCAAGCAGGCTGGATTCTGGATGCG 420  
QY 421 ATCCCTGAGACCGGTGAGCAGGCTCTGAGATCCAGACCTGGGATCACCCAGACAC 480  
DB 421 ATCCCTGAGACCGGTGAGCAGGCTCTGAGATCCAGACCTGGGATCACCCAGACAC 480  
QY 481 GTCAATTGTGATGCTCCAGACAGCTCTGATCGAGAGAACTTGGGGAAGAAATC 540  
DB 481 GTCAATTGTGATGCTCCAGACAGCTCTGATCGAGAGAACTTGGGGAAGAAATC 540  
QY 541 GACCTCAAACTGGAGAGATTATCACACCACTTTGACTGGCCACCGAATCTGAATC 600  
DB 541 GACCTCAAACTGGAGAGATTATCACACCACTTTGACTGGCCACCGAATCTGAATC 600  
QY 601 CAGAACCGTCTCATGTGTCAGAGGACATCTCAGCTGGAGCGGCTCAGAACTG 657  
DB 601 CAGAACCGTCTCATGTGTCAGAGGACATCTCAGCTGGAGCGGCTCAGAACTG 657

RESULT 11  
BU617945/c  
LOCUS  
DEFINITION  
UI-H-DF0-beu-d-15-0-UI.s1 NCI CGAP.DF0 Homo sapiens cDNA clone  
UI-H-DF0-beu-d-15-0-UI 3', mRNA sequence.  
BU617945  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BU617945 721 bp mRNA linear EST 23-SEP-2002  
UI-H-DF0-beu-d-15-0-UI.s1 NCI CGAP.DF0 Homo sapiens cDNA clone  
UI-H-DF0-beu-d-15-0-UI 3', mRNA sequence.  
BU617945  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source

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/db\_xref="taxon:9606"  
/clone="UI-H-DF0-beu-d-15-0-UI"  
/tissue\_type="Subchondral Bone"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI CGAP.DF0"  
/note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; NCI CGAP.DF0 is a cDNA library containing the following tissue(s): Subchondral Bone. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTTACGCTC.  
TAG TISSUE=Subchondral bone  
TAG LIB=UI-H-DF0  
TAG\_SEQ=GTTAAGCGTC"

ORIGIN

Query Match 41.0%; Score 591; DB 5; Length 721;  
Best Local Similarity 99.7%; Pred. No. 1.4e-146;  
Matches 591; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 848 TGCAGGCGCCCTCTCTGGCCAGAAATACAGGCTTGTCAATGTCTCTGTGGCAACTGC 907  
DB 719 TGCAGGCGCCCTCTCTGGCCAGAAATACAGGCTTGTCAATGTCTCTGTGGCAACTGC 650  
QY 908 TGAAGAGGCTGTGGCAGATAGGACACAGTTGGCGAGCTCATCCAGCCCTCTTTGAAA 967  
DB 659 TGAAGAGGCTGTGGCAGATAGGACACAGTTGGCGAGCTCATCCAGCCCTCTTTGAAA 600  
QY 968 AGGAGATGGCAGTTCTTCAGACAGCTCTCATGAGGTGCTGAGCCAGCGCTGACACAGC 1027  
DB 599 AGGAGATGGCAGTTCTTCAGACAGCTCTCATGAGGTGCTGAGCCAGCGCTGACACAGC 540  
QY 1028 AGGACTGATCCAGAAAGGCTGGGTGTCTACCGCGCTCCCGCGGAGCTCGACAGGCAC 1087





Mon Mar 21 09:11:06 2005

Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,  
Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Bruscia,V.A.,  
Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,  
Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,  
Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,  
Gutencich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,  
Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,  
Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,  
Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,  
Numata,K., Okido,T., Pavan,W.J., Perle,G., Pesole,G.,  
Petrowsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,  
Verardo,R., Wagner,L., Wallestedt,C., Wang,Y., Watanabe,Y., Yang,I.,  
Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,  
Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,  
Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,  
Verardo,R., Wagner,L., Wallestedt,C., Wang,Y., Watanabe,Y., Yang,I.,  
Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,  
Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,  
Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,  
Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,  
Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,  
Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,  
Rogers,J., Birney,E. and Hayashizaki,Y.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
22354683  
12466851  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/  
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,  
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,  
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,  
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,  
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,  
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,  
Takeda,Y., Waki,K., Watanishi,A., Muramatsu,M. and Hayashizaki,Y.  
Direct Submission  
Computational Analysis of Full-length Mouse cDNAs Compared with  
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
10 (11), 1757-1771 (2000)  
Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site (http://genome.gsc.riken.go.jp) for  
further details.  
Location/Qualifiers  
1. .996  
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/mol\_type="mRNA"  
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whole body"

ORIGIN		Query Match	36.0%	Score 518.4	DB 6	Length 996
		Best Local Similarity	76.4%	Pred. No. 4.2e-127		
		Matches 636	Conservative	0	Mismatches 196	Indels 0
		Gaps 0				
QY	1	ATGAGCGCACTATCGCCCGCCGACCGGTATCCCGCCGAGATGCCCGAGTACGGGGAGGAG	60			
DB	26	ATGGATGCAACACACAGCCCTCATCGCATTTCCCGGAAATGCTCAGTAGGGGAGAC	85			
QY	61	AACACATCTTCGAGTTGATGCAAAATGCTGGAGCAATCTCTGATCCACCGCCGAA	120			
DB	86	TACTACATTTTCGAGATGATGCAAAATGCTGGAGCAATCTCTGATCCACCGCCGAG	145			
QY	121	GATCCCATCCCTTCATGATCCAGCATTTGCAATGAGACACAGCATGTGCCAGATT	180			
DB	146	GACCCCATCAGCTTCATGATCACTCACCTGCGCAGGAACATGATGATGTCGCAAGTGT	205			
QY	181	GTAATATTAGTTCACCGCTTCAGGGAACAAATAGCAATGTGGCTCTGCAAAACAT	240			
DB	206	GTGATATTAGTTCGCGCTTCAGGGAACAAATAGCAATGTGGCTCTGCAAAACAT	265			
QY	241	CTGAACAGCAGTCTCTCTCACCTCTGAGAACCTGATCTTTAAATGATGTTTTCTATACGCC	300			
DB	266	CTAACACGCACTCATCAACAGGAGAGCTTACTAGAAAGAGAGATTTTCCCGTCTGTCT	325			
QY	301	ACCGAAGCCAGAGCGTTTATCTGCAAGGAGAGCAGTTTCCAGCGCGCTCTGCTCCAG	360			
DB	326	GTGGAAGCCAGAGTTACTTACCGAGTTTACGAAGAATTCGATTCGATTTCTGTCAGT	385			
QY	361	CTGATTTCAGAACCGCTTCGCTGAAGAGGATTCATCAACAGCGGCTGATTCGATGCGC	420			
DB	386	CTTGTCAGAGCGCTTCGATGAAGATGACTGCCTCAGAAAGGCTGATCTCGACCGC	445			
QY	421	ATCCCTGAGACCGCTGAGCAGGCTCTGAGGATCCAGCCCTGGGATCACCCAGACAC	480			
DB	446	ATCCCTGAGAGCGCGGAGCAGGCTCTGATGATCCAGACCCCTGGGCTGGGCCAGAC	505			
QY	481	GTGATTGCTCAGTGCTCCAGACACCGTTCCTGATCGAGAGAAATCTGGGGAAGAATC	540			
DB	506	GTGATTGCTCAGTGCTCCAGACACCGTTCCTGATCGATGAGAAATGTTGGGGAAGCGGATC	565			
QY	541	GACCTCTCAAATGGAGAGATTTATCACACCTTTGATGCGCCCGCCGCAATCTGAAATC	600			
DB	566	GACCTCTCAACGGAGAGATCTATCACACCTTTGATGCGCCCGCCGCAATCTGAAATC	625			
QY	601	CAGAACCGCTCATGCTGCGCAGAGGACATCTCAGAGCTGAGAGACGCTCAGAAATCTGCTG	660			
DB	626	CAGAACCGCTGAGACAGCGGAGGAGCATCTCGAGATCGAAACGGGGAAGAAGCTGCTG	685			
QY	661	GAGTATCATAGGAACATCGTTCAGGGTTCATTCGCTCTTACCCCAAAATCTCAAGTCATC	720			
DB	686	GAGTATCATAGGAACATCATCATCAGGATCTTCTCTTCTTACCCCAAAATCTCAAGTCATC	745			
QY	721	AGTGTGACAGCAGCATGTTGGAGCGTCTTCTACAGCGCTCTGACCTATGTCCAAAGCAAC	780			
DB	746	AGCTCAGACAGCGGCTGTTGGATGCTTCTTACAGGCTCTGACCTATGTGCAATCTGGG	805			
QY	781	CATCGTACTAATGCCCGTTTCAACCGGAGGCTGCTGCTGCTGGGCTGTGG	832			
DB	806	CATCGATGCTATGCTCCATTCACCCCGGAGGTGCTGCTGCTGGGCGCTTGG	857			

RESULT 14	BP368808	550 bp	mRNA	linear	EST 17-SEP-2004
LOCUS	BP368808	Sugano cDNA library, testis	Homo sapiens	cDNA clone	
DEFINITION	TS100249, mRNA sequence.				
ACCESSION	BP368808				
VERSION	BP368808.1	GI:52299075			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				



ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 550)  
AUTHORS Suzuki.Y., Yamashita.R., Shiota.M., Sakakibara.Y., Chiba.J.,  
Mizushima-Sugano.J., Nakai.K. and Sugano.S.  
TITLE Sequence comparison of human and mouse genes reveals a homologous  
block structure in the promoter regions  
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)  
COMMENT Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp.  
FEATURES  
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/organism="Homo sapiens"  
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ORIGIN  
Query Match 35.7%; Score 514.2; DB 5; Length 550;  
Best Local Similarity 99.4%; Pred. No. 4.6e-126;  
Matches 516; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 ATGGAGCGCCACTATCGCCCGCCACCGTATCCCCCGGAGATGCCCACTACGGGGAGGAG 60  
DB 32 ATGGAGCGCCACTATCGCCCGCCACCGTATCCCCCGGAGATGCCCACTACGGGGAGGAG 91  
QY 61 AACCACTCTTCGAGTTGATGCAGACATGCTGGAGCACTCTGATCCACAGCCCGAA 120  
DB 92 AACCACTCTTCGAGTTGATGCAGACATGCTGGAGCACTCTGATCCACAGCCCGAA 151  
QY 121 GATCCATCCCTTCATGATCGAGCATCTGCATAGAGCAAGCAATGTGCCAGGATT 180  
DB 152 GATCCATCCCTTCATGATCGAGCATCTGCATAGAGCAAGCAATGTGCCAGGATT 211  
QY 181 GTAATATTAGTCCACCGCCTCAGGAAACCAATAGCAATGTGGCTCTGCAAAAT 240  
DB 212 GTAATATTAGTCCACCGCCTCAGGAAACCAATAGCAATGTGGCTCTGCAAAAT 271  
QY 241 CTGAACAGCAGTCTCTCACCCTGGAGAACCTGATCTTAATGAGTTTCTATAGGCC 300  
DB 272 CTGAACAGCAGTCTCTCACCCTGGAGAACCTGATCTTAATGAGTTTCTATAGGCC 331  
QY 301 ACCGAGCGCAGAGGCTTTATCTGCAAGGAGACAGTTCCAGCGGCTGCTGTCAG 360  
DB 332 ACCGAGCGCAGAGGCTTTATCTGCAAGGAGACAGTTCCAGCGGCTGCTGTCAG 391  
QY 361 CTGATTGAGGAACGCTGCTGAGAGGATTCATCAAGCAGGCTGGATTCTGGATGCC 420  
DB 392 CTGATTGAGGAACGCTGCTGAGAGGATTCATCAAGCAGGCTGGATTCTGGATGCC 451  
QY 421 ATCCCTGAGACGCGTGAGCAGGCTCTGAGGATCCAGACCTGGGGATCACCCAGAC 480  
DB 452 ATCCCTGAGACGCGTGAGCAGGCTCTGAGGATCCAGACCTGGGGATCACCTCAGAC 511  
QY 481 GTCATTGTCTGAGTGCTCCACACAGGCTCTGATCGAG 519  
DB 512 GTCATTGTCTGAGTGCTCCACACAGGCTCTGATCGAG 550

RESULT 15  
LOCUS BP347783  
DEFINITION BP347783 Sugano cDNA library, brain Homo sapiens cDNA clone  
S2B06383, mRNA sequence.  
ACCESSION BP347783  
VERSION BP347783.1 GI:52277768  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 583)  
AUTHORS Suzuki.Y., Yamashita.R., Shiota.M., Sakakibara.Y., Chiba.J.,  
Mizushima-Sugano.J., Nakai.K. and Sugano.S.  
TITLE Sequence comparison of human and mouse genes reveals a homologous  
block structure in the promoter regions  
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)  
COMMENT Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp.  
FEATURES  
source  
1..583  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="SZB06383"  
/tissue type="brain"  
/clone\_lib="Sugano cDNA library, brain"

ORIGIN  
Query Match 35.7%; Score 513.8; DB 5; Length 583;  
Best Local Similarity 98.9%; Pred. No. 8e-126;  
Matches 548; Conservative 0; Mismatches 3; Indels 3; Gaps 3;  
QY 1 ATGAGCCGCACTAT-CCGCCCCGACCGTATCCCCCGGAGATCCCCAGTACGGGGAGGA 59  
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QY 60 GAACCACTCTTCGAGTTGATGCAGAACATGCTGGAGCAACTCTCTGATCCACAGCCGA 119  
DB 90 GAACCACTCTTCGAGTTGATGCAGAACATGCTGGAGCAACTCTCTGATCCACAGCCGA 149  
QY 120 AGATCCCATCCCTTTCATGATCCAGCACTTGCATAGAGCAAGCAATGTGCCAGGAT 179  
DB 150 AGATCCCATCCCTTTCATGATCCAGCACTTGCATAGAGCAAGCAATGTGCCAGGAT 209  
QY 180 TGTAAATATTAGTCCACCGCCTCAGGAAACCAATAGCAATGTGGCTCTGCAAAACA 239  
DB 210 TGTAAATATTAGTCCACCGCCTCAGGAAACCAATAGCAATGTGGCTCTGCAAAACA 269  
QY 240 TCTGAACAGCAGTCTCTCACCCTGGAGAACCTGATCTTAAATGAGTTTCTATACGCC 299  
DB 270 TCTGAACAGCAGTCTCTCACCCTGGAGAACCTGATCTTAAATGAGTTTCTATACGCC 329  
QY 300 CACCGAAGCCAGAGGCTTTATCTGCAAGGAGACAGTTCCAGCGGCTGCTGTCACA 359  
DB 330 CACCGAAGCCAGAGGCTTTATCTGCAAGGAGACAGTTCCAGCGGCTGCTGTCACA 389  
QY 360 GCTGATTTCAGGAACGCTGCTGAGAGGATTCG-ATCAAGCAGGG-CTGGATTCTGGAT 417  
DB 390 GCTGATTTCAGGAACGCTGCTGAGAGGATTCGATCAAGCAGGAGCTGGATTCTGGAT 449  
QY 418 GGCATCTCTGAGACGCGTGAGCAGGCTCTGAGGATCCAGACCTGGGGATCACACCCAGA 477  
DB 450 GGCATCTCTGAGACGCGTGAGCAGGCTCTGAGGATCCAGACCTGGGGATCACACCCAGA 509  
QY 478 CACGTCATTGTCTGAGTGCTCCAGACACGCTCTCTGATCGAGAGAAAATTGGGGAAGAGA 537  
DB 510 CACGTCATTGTCTGAGTGCTCCAGACACGCTCTCTGATCGAGAGAAAATTGGGGAAGAGA 569  
QY 538 ATCGACCTCTCAAC 551  
DB 570 ATCGACCTCTCANAC 583

Search completed: March 19, 2005, 23:48:58  
Job time : 4394 sec

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GenCore version 5.1.6

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 19, 2005, 19:05:28 ; Search time 775 Seconds  
(without alignments)

**Title:** US-10-798-773-1

Accession: [U00001](#)  
 US-10-198-713-1  
 Perfect score: 1440  
 Sequence: 1 atggagcgccactatgcggcc.....tgccaaagaaatccccctca 1440

Scoring table: IDENTITY NUC

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

**Database :**

1: N\_Geneseq\_15Dec04:\*  
 2: geneseqm1980s:\*  
 3: geneseqm1990s:\*  
 4: geneseqm2000s:\*  
 5: geneseqm2001bs:\*  
 6: geneseqm2001bs:\*  
 7: geneseqm2002bs:\*  
 8: geneseqm2002bs:\*  
 9: geneseqm2003bs:\*  
 10: geneseqm2003bs:\*  
 11: geneseqm2003ds:\*  
 12: geneseqm2004bs:\*  
 13: geneseqm2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES									
Result No.	Score	Query		DB	ID	Description			
		Match	Length						
1	1440	100.0	1440	10	ABV75301	Abv75301 Novel hum			
2	1440	100.0	1579	8	ADB53813	ADB53813 Human cod			
3	1440	100.0	1581	8	ADP53173	Adp53173 Human kin			
4	1394	96.8	1623	10	ADC10109	Adc10109 Human NOV			
5	1170	81.2	1619	10	ADB63503	Adb63503 Human CDN			
6	1166	81.0	1987	10	ADC10107	Adc10107 Human NOV			
7	1032.8	71.7	1452	4	ADL14324	Adl14324 Human 278			
8	1032.8	71.7	1452	4	AAS61170	Aas61170 Human 278			
9	1027.6	71.4	1223	4	AAS27222	Aas27222 cDNA enco			
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11	868	60.3	995	6	ADB26472	Adb26472 Human kin			
12	761	52.8	1778	4	AAI58051	Aai58051 Human pol			
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14	574	39.9	615	6	ABK71537	Abk71537 Human dit			
15	463.4	32.2	997	4	AAK51550	Aak51550 Human pol			
16	461.8	32.1	809	4	AAK52534	Aak52534 Human pol			
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18	407	28.2	407	9	ACH29455	Ach29455 Human adu			
19	366.6	25.3	447	9	ACH41952	Ach41952 Human foe			
20	322	22.4	509	4	AAS27220	Aas27220 cDNA enco			

## ALIGNMENTS

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ID	ABV75301 standard; DNA; 1440 BP.
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XX	ABV75301;
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XX	07-MAR-2003 (first entry)
DT	
XX	
XX	Novel human kinase polypeptide (NHP) encoded
DE	
XX	NHP; kinase; gene therapy; drug screening
KW	
XX	Homo sapiens.
XX	
XX	Key
FH	Location/Qualifiers
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FT	/product= "NHP"
FT	/note= "Kinase polypeptide"
FT	
XX	
XX	WO200290517-A2.
PN	
XX	
XX	14-NOV-2002.
PD	
XX	
XX	08-MAY-2002; 2002WO-US014669.
PF	
XX	
XX	09-MAY-2001; 2001US-0289727P.
PR	
XX	(LEXI-) LEXICON GENETICS INC.
PA	
XX	
XX	Yu X, Xie Q, Abuin A, Walke DW;
PI	
XX	
XX	WPI; 2003-103514/09.
DR	
DR	P-PSDB; ABB82701.
XX	
XX	New human kinase proteins and polynucleotide
PT	nutriceutical applications, drug screening,
PT	diagnosing or treating diseases associated
PT	imbalances.
PT	
XX	
PS	Claim 1; Page 38; 40pp; English.
XX	
XX	The invention relates to novel human polypep
CC	

CC	activity and polynucleotides encoding them. The polynucleotides,
CC	proteins, antibodies, agonists and antagonists of the proteins are useful
CC	for drug screening, clinical trial monitoring, and diagnosis or treating
CC	diseases or disorders associated with biological disorders or imbalances.
CC	The proteins and polynucleotides are useful in cosmetic and nutraceutical
CC	applications, for identifying protein coding sequences and mapping a
CC	unique gene to a particular chromosome. The sequence of the
CC	polynucleotides and proteins can also be used as additional DNA markers
CC	for restriction fragment length polymorphism analysis, or in forensic
CC	biology. The present sequence represents a NHP kinase encoding DNA
XX	
SQ	Sequence 1440 BP; 368 A; 419 C; 367 G; 286 T; 0 U; 0 Other;
	Query Match 100.0%; Score 1440; DB 10; Length 1440;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 1440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ATGAGCGGCACTATCGGCCCGCCACCGTATCCCCCGAGATGCCCGAGTACGGGGAGGAG 60
DB	1 ATGAGCGGCACTATCGGCCCGCCACCGTATCCCCCGAGATGCCCGAGTACGGGGAGGAG 60
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DB	61 AACCACTTTGAGTTGATGACAGAACATGCTGGAGCAACTCTCTGATCCACCGCCGAA 120
QY	121 GATCCATCCCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB	121 GATCCATCCCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
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DB	241 CTGAACAGAGTCTCTCACTCTGAGAACCTGATCTTAATGATGTTTCTCTATACGCC 300
QY	301 ACCGAAGCCAGAGGCTTTATCTGCAAGAGGAGACAGTCTCCAGCGGCTGCTCGTCCAG 360
DB	301 ACCGAAGCCAGAGGCTTTATCTGCAAGAGGAGACAGTCTCCAGCGGCTGCTCGTCCAG 360
QY	361 CTGATTCAGGAACCGCTGGCTGAAAGAGTTCATCAGCAGGCTGGATTCGATGTCGG 420
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QY	421 ATCCCTTGAGACCGCTGAGCAGGCTCTGAGGATCCAGACCTCTGGGATCACACCGAC 480
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DB	481 GTCAATTTGCTGAGTCTCCAGACACGCTCTGATGAGAGAACTTGGGAGAGATC 540
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DB	541 GACCTTCAAACTGGAGAGTTTATCACACCTTTGATGAGGACCCCGAATCTGAAATC 600
QY	601 CAGAACCGTCTCATGCTGCGCAGAGGACATCTCAGAGCTGGAGACGGCTCAGAAATCTG 660
DB	601 CAGAACCGTCTCATGCTGCGCAGAGGACATCTCAGAGCTGGAGACGGCTCAGAAATCTG 660
QY	661 GAGTATCATAGGAACATCGTCAGGGTCATTCCCTTACCCCAAAATCTCAAGTCATC 720
DB	661 GAGTATCATAGGAACATCGTCAGGGTCATTCCCTTACCCCAAAATCTCAAGTCATC 720
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QY	781 CATCGTACTAATGCCCGGTTTACCCCCAGGGTCTGCTGCTCGGGCTGTTGGGAGTGGG 840
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QY	841 AAAAGTCTGACGGCGCCCTCTCTGGCCAGAAATACAGGCTTCTCAATGCTCTGCTGGG 900
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DB	1021 GACCAAGAGGAGTGCATCCAGAAAGGCTGGTGTCTACACGCGCTCCCGCGGAGCTCGAC 1080
QY	1081 CAGGCACACCTGCTGAACCGGCTGGGCTTACAAATCCCAACAGGGTGTCTTCTGAATGTG 1140
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QY	1321 GCTGACTTGGAGCAGTGTGTGAGGCTGGCCATCACCTCAATGGGAGCAGGACCCATAC 1380
DB	1321 GCTGACTTGGAGCAGTGTGTGAGGCTGGCCATCACCTCAATGGGAGCAGGACCCATAC 1380
QY	1381 ACAGTCTTCCAAATACATCGAGAGTGGGATCAATTAATCCCTGCCCCAAGAAATCCCTGA 1440
DB	1381 ACAGTCTTCCAAATACATCGAGAGTGGGATCAATTAATCCCTGCCCCAAGAAATCCCTGA 1440

RESULT 2

ADAS3813  
ID ADAS3813 standard; cDNA; 1579 BP.

XX ADAS3813;

XX 20-NOV-2003 (first entry)

XX Human coding sequence, SEQ ID 1381.

XX Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;  
XX Gene Therapy; human; secretory protein; membrane proteins; cancer;  
XX inflammatory disease; osteoporosis; neurological disease; gene; ss.

XX Homo sapiens.

XX EP1293569-A2.

XX 19-MAR-2003.

XX 21-MAR-2002; 2002EP-00006586.

XX 14-SEP-2001; 2001JP-00328381.

XX 24-JAN-2002; 2002US-0350435P.

XX (HELI-) HELIX RES INST.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;

XX Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;

XX Seki N, Yoshikawa T, Otsuka M, Nagahara K, Masuho Y;

XX

DR WPI; 2003-395539/38.  
 XX P-PSDB; ADA5452.  
 PT New polynucleotides encoding full-length polypeptides, e.g. secretory  
 PT and/or membrane proteins, useful for developing medicines for diseases in  
 XX which the gene is involved, or as target molecules for gene therapy.  
 XX Claim 1; SEQ ID NO 1381; 205pp; English.  
 XX The present invention relates to novel human secretory or membrane  
 CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-  
 CC ADA54071). The coding sequences are useful in the gene therapy of  
 CC diseases caused by abnormalities of the proteins, e.g. cancer,  
 CC inflammatory diseases, osteoporosis or neurological disease.  
 XX Sequence 1579 BP; 403 A; 467 C; 406 G; 303 T; 0 U; 0 Other;

Query Match 100.0%; Score 1440; DB 10; Length 1579;  
 Best Local Similarity 100.0%; Pred. No. 0;  
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Qy 1 ATGGAGCGCACTATCGCCCGCCGACCGTATCCCGCCGAGATGCCCGAGTACGGGAGGAG 60  
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 Db 90 AACCAATCTTCGAGTTGATGACAGAACATGCTGGAGCACTCTGATCCACCGCCGAA 149  
 Qy 121 GATCCCATCCCTTCATGTCAGCACTTGCAATAGAGCAACAAATGTGCCAGGATT 180  
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 Qy 241 CTGAACAGCAGTCTCTCACCCTGAGAGCACTGATCTTAATGAGTTTCTTATAGGCC 300  
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 Db 330 ACCGAAGCCAGAGGCTTATCTGCAAGGAGAGACAGTTCGACGGGCTGTCTGTCAG 389  
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 Db 510 GTCAATTGCTGAGTCTCCACACAGGCTCTGATCGAGAGAACTTGGGAGAGAAATC 569  
 Qy 541 GACCTCAAACTGGAGAGATTATCAACCACTTTGACTGGCCACCCGAAATCTGAAATC 600  
 Db 570 GACCTCAAACTGGAGAGATTATCAACCACTTTGACTGGCCACCCGAAATCTGAAATC 629  
 Qy 601 CAGAACCGTCTCATGTTGCCAGAGACATCTCGAGCTGGAGACGGCTCAGAAATCTGCTG 660  
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 Qy 721 AGTGCTGACCGCAATGTGGAGCTTCTACAGGCTCTGACCTATGTCCAAAGCAAC 780  
 Db 750 AGTGCTGACCGCAATGTGGAGCTTCTTACAGGCTCTGACCTATGTCCAAAGCAAC 809

Qy 781 CATCTACTAATAGCCCGTTACCCGAGGGTCTGCTGCTCGGGCTGTGGGCAGTGGG 840  
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 Db 870 AAAAGTCTGAGCGCGCCCTCTCGGCCAGAAATACAGGCTTGTCAATGTCTGTGGG 929  
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 Db 930 CAACTGCTGAAAGAGGCTGTGGCAGATAGGACACAGTTTGGCGAGCTCATCCAGCCCTTC 989  
 Qy 961 TTTGAAAAGAGGATGGCAGTTCTGACAGCTCTCATGAGGTGTGAGCGAGCGCTG 1020  
 Db 990 TTTGAAAAGAGGATGGCAGTTCTGACAGCTCTCATGAGGTGTGAGCGAGCGCTG 1049  
 Qy 1021 GACCAGCAGGACTGCATCCAGAAAGCTGGGTGCTTACACGGCTGCCGGGAGCTTCGAC 1080  
 Db 1050 GACCAGCAGGACTGCATCCAGAAAGCTGGGTGCTTACACGGCTGCCGGGAGCTTCGAC 1109  
 Qy 1081 CAGGCACACTGCTGTAACCCGCTGGGCTACAATCCCAACAGGGTGTCTTCTGAAATGTG 1140  
 Db 1110 CAGGCACACTGCTGTAACCCGCTGGGCTACAATCCCAACAGGGTGTCTTCTGAAATGTG 1169  
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 Db 1170 CCATTGATTCCATCATGAGCGGCTGACTCTGAGAAAGAAATTCATCCAGTCACTGGGNA 1229  
 Qy 1201 AGGTACCACCTCATGTACAGCCACCTCCGACCATGGAGATCCAGGCTGCTCTCTGAG 1260  
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 Db 1350 GCTGACTTGGAGCAGTGTGTATGGGTTCGGGCTCAACCTCAATGGGAGCCAGGACCATAC 1409  
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 Db 1410 ACAGTCTTCGAAATACATCGAGGTGGGATCATTAATCCCTGCCCAAGAAATCCCTGA 1469

RESULT 3  
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 ID AAD53173 standard; cDNA; 1581 BP.  
 XX AAD53173;  
 AC AAD53173;  
 XX 28-MAY-2003 (first entry)  
 DT 28-MAY-2003 (first entry)  
 XX Human kinases and phosphatases (KPP) -3 cDNA.  
 DE Human; kinase and phosphatase; KPP; enzyme; cardiovascular disorder;  
 XX Human; kinase and phosphatase; KPP; enzyme; cardiovascular disorder;  
 KW neurological disorder; cancer; gene therapy; gene; ss.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 15..1454  
 FT /\*tag= a  
 FT /product= "KPP protein"  
 XX  
 XX WO200294780-A2.  
 XX 28-NOV-2002.  
 XX 23-MAY-2002; 2002WO-US016634.  
 XX 24-MAY-2001; 2001US-0293665P.  
 XX 15-JUN-2001; 2001US-0298712P.

Mon Mar 21 09:11:05 2005

PR 06-JUL-2001; 2001US-0303418P.  
PR 19-JUL-2001; 2001US-0306967P.  
PR 27-JUL-2001; 2001US-0308183P.  
PR 15-DEC-2001; 2001US-0343007P.  
PR 15-FEB-2002; 2002US-0357675P.  
PR 30-APR-2002; 2002US-0376988P.  
XX  
XX (INCY-) INCYTE GENOMICS INC.  
XX Yue H, Lu DAM, Azimzai Y, Ding L, Lee EA, Hafalia AJA, Becha SD;  
XX Tang YT, Lal PG, Griffin JA, Gururajan R, Ramkumar J, Elliott VS;  
XX Arvizu CS, Luo W, Swarnakar A, Duggan BM, Tran UK, Walia NK;  
XX Gandhi AR, Yao MG, Khan FA, Raughn WR, Borowsky ML, Zebarjadian Y;  
XX Richardson TW, Marquis JP, Chien D, Jin P;  
XX WPI; 2003-120774/11.  
XX P-PSDB; AAE34860.  
XX New human kinases and phosphatases (KPP), useful for preparing a  
XX composition for diagnosing or treating a disease or condition associated  
XX with decreased expression or overexpression of functional KPP e.g.,  
XX cancer.  
XX Claim 5; Col 154; 82pp; English.  
XX The invention relates to novel human kinases and phosphatases (KPP)  
XX polypeptides and polynucleotides. Polypeptides of the invention are used  
XX for screening agonists and antagonists. They are used to make monoclonal  
XX or polyclonal or antibodies, which are used in diagnostic tests for  
XX conditions or diseases associated with expression of the polypeptide.  
XX They are also useful for diagnosing or treating diseases or conditions  
XX associated with decreased expression or overexpression of functional KPP  
XX e.g. cardiovascular or neurological disorders or cancer. The invention is  
XX useful in gene therapy. The present sequence is human KPP cDNA  
XX  
XX Sequence 1581 BP; 413 A; 464 C; 402 G; 302 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 1440; DB 8; Length 1581;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGAGCGCACTATGCGCCGCGCAGCGTATCCCGCGAGATGCCCGATCGGGGAGGAG 60  
DB 15 ATGGAGCGCACTATGCGCCGCGCAGCGTATCCCGCGAGATGCCCGATCGGGGAGGAG 74  
QY 61 AACCACTCTCGAGTTGATGAGAACATGCTGGAGCAACTCTGATCCACCGCCGAA 120  
DB 75 AACCACTCTCGAGTTGATGAGAACATGCTGGAGCAACTCTGATCCACCGCCGAA 134  
QY 121 GATCCCATCCCTTCATGATCCAGCACTTGGCATAGAGACAGCAATGTGCCAGGATT 180  
DB 135 GATCCCATCCCTTCATGATCCAGCACTTGGCATAGAGACAGCAATGTGCCAGGATT 194  
QY 181 GTAAATATTAGTCCACCGCTCAGGAAACAAATAGCAATGTGGCTCTGCAAAACAT 240  
DB 195 GTAAATATTAGTCCACCGCTCAGGAAACAAATAGCAATGTGGCTCTGCAAAACAT 254  
QY 241 CTGAACAGCAGTCTCTCTACCCCTGGAGAACCTGATCTTAAATGAGTTTCTATACGCC 300  
DB 255 CTGAACAGCAGTCTCTCTACCCCTGGAGAACCTGATCTTAAATGAGTTTCTATACGCC 314  
QY 301 ACCGAGCCGAGAGGCTTTATCTGCAAGAGACAGTCCCGCGCGCTGCTCTCCAG 360  
DB 315 ACCGAGCCGAGAGGCTTTATCTGCAAGAGACAGTCCCGCGCGCTGCTCTCCAG 374  
QY 361 CTGATTCAGGAACGCTTGGCTGAAGAGATTGATCAAGCAGCGGCTGGATTCTGGATGCG 420  
DB 375 CTGATTCAGGAACGCTTGGCTGAAGAGATTGATCAAGCAGCGGCTGGATTCTGGATGCG 434  
QY 421 ATCCCTGAGACGGCTGAGAGGCTCTGAGGATCCAGACCTGGGATCACACGACAC 480  
DB 435 ATCCCTGAGACGGCTGAGAGGCTCTGAGGATCCAGACCTGGGATCACACGACAC 494

QY 481 GTCAATGTGTGAGTGTCTCAGACACGGTCTCTGATCGAGAGAACTTGGGAGAGAAATC 540  
DB 495 GTCAATGTGTGAGTGTCTCAGACACGGTCTCTGATCGAGAGAACTTGGGAGAGAAATC 554  
QY 541 GACCTCAAACTGGAGAGATTATACACACCACTTTGACTGGCCACCCGAATCTGAAATC 600  
DB 555 GACCTCAAACTGGAGAGATTATACACACCACTTTGACTGGCCACCCGAATCTGAAATC 614  
QY 601 CAGAACCGTCTCATGGTCCAGAGGACATCTCAGAGCTGGAGAGCGCTCAGAACTGCTG 660  
DB 615 CAGAACCGTCTCATGGTCCAGAGGACATCTCAGAGCTGGAGAGCGCTCAGAACTGCTG 674  
QY 661 GAGTATCATAGACATGCTCAGGGTCAATCCCTCTACCCCAAAATCTCAAAGTCAATC 720  
DB 675 GAGTATCATAGGAAACATGCTCAGGGTCAATCCCTCTACCCCAAAATCTCAAAGTCAATC 734  
QY 721 AGTGTCTGACCAACCATGCTGTGGAGCTCTTCTACCAAGGCTCTGACCTATGTCCAAAGCAAC 780  
DB 735 AGTGTCTGACCAACCATGCTGTGGAGCTCTTCTACCAAGGCTCTGACCTATGTCCAAAGCAAC 794  
QY 781 CATCTACTAATGCGCCGTTTCAACCCGAGGGTGTCTGCTCCGGGCTGTGGGCGAGTGGG 840  
DB 795 CATCTACTAATGCGCCGTTTCAACCCGAGGGTGTCTGCTCCGGGCTGTGGGCGAGTGGG 854  
QY 841 AAAAGTCTGCGAGCGCCCTCTCTGCGCCAGAAATACAGGCTTGTCAATGTCTGTGTGGG 900  
DB 855 AAAAGTCTGCGAGCGCCCTCTCTGCGCCAGAAATACAGGCTTGTCAATGTCTGTGTGGG 914  
QY 901 CAACTGCTGAAAGAGGCTGTGGCAGATAGGACCAAGTTTGGCGAGCTCATCCAGCCCTTC 960  
DB 915 CAACTGCTGAAAGAGGCTGTGGCAGATAGGACCAAGTTTGGCGAGCTCATCCAGCCCTTC 974  
QY 961 TTTGAAAAGAGAGATGGCAGTTCCTCAGACGCTCTCTCATGAAGTGTCTGAGCAGCGCTG 1020  
DB 975 TTTGAAAAGAGAGATGGCAGTTCCTCAGACGCTCTCTCATGAAGTGTCTGAGCAGCGCTG 1034  
QY 1021 GACCAAGCAGGACTGCATCCAGAAAGGCTGGGTGTCTACACGGGCTCCCGGGGACCTCGAC 1080  
DB 1035 GACCAAGCAGGACTGCATCCAGAAAGGCTGGGTGTCTACACGGGCTCCCGGGGACCTCGAC 1094  
QY 1081 CAGGCAACCTGTGTGAACCGCTGGGCTACATCCCAAGGCTGTTTCTCTGAATGTG 1140  
DB 1095 CAGGCAACCTGTGTGAACCGCTGGGCTACATCCCAAGGCTGTTTCTCTGAATGTG 1154  
QY 1141 CCATTTGATTCCATCATGAGCGGCTGACTCTGAGAGAAATGATCCAGTCACTGGGAA 1200  
DB 1155 CCATTTGATTCCATCATGAGCGGCTGACTCTGAGAGAAATGATCCAGTCACTGGGAA 1214  
QY 1201 AGGTACCACTCATGTACAAAGCACTCCCAAGGAGATCCAGGCTCGCTCTCTGAG 1260  
DB 1215 AGGTACCACTCATGTACAAAGCACTCCCAAGGAGATCCAGGCTCGCTCTCTGAG 1274  
QY 1261 AACCCAAAGGATGCTCAAGAGCAGGCTCAAGCTGAAATGGAGCTGTTCTACAGGAATCA 1320  
DB 1275 AACCCAAAGGATGCTCAAGAGCAGGCTCAAGCTGAAATGGAGCTGTTCTACAGGAATCA 1334  
QY 1321 GCTGACTTTGAGCAGTGTGATGGGTGGGCAATCAACCTCAATGGGACCAAGGACCCATAC 1380  
DB 1335 GCTGACTTTGAGCAGTGTGATGGGTGGGCAATCAACCTCAATGGGACCAAGGACCCATAC 1394  
QY 1381 ACAGTCTTCAATACATCGAGAGTGGGATCAATTAATCCCTGCCCAAGAAATCCCTCTGA 1440  
DB 1395 ACAGTCTTCAATACATCGAGAGTGGGATCAATTAATCCCTGCCCAAGAAATCCCTCTGA 1454

RESULT 4  
ADCl0109 standard; DNA; 1623 BP.  
ID ADCl0109  
XX  
AC ADCl0109;  
XX  
DT 18-DEC-2003 (first entry)  
XX

Human NOVX polypeptide coding sequence SEQ ID NO: 129.

ds; gene; cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective; antiinflammatory; gene therapy; antisense therapy; thrombolytic; NOVX; pathology; cancer; diabetes; obesity; thrombotic disorder; CNS disorder; inflammatory disorder; chromosome mapping; tissue typing; predictive medicine.

Homo sapiens.

WO2003000842-A2.

03-JAN-2003.

04-JUN-2002; 2002WO-US017443.

04-JUN-2001; 2001US-0295607P.

04-JUN-2001; 2001US-0295661P.

06-JUN-2001; 2001US-0296404P.

06-JUN-2001; 2001US-0296418P.

07-JUN-2001; 2001US-0296575P.

11-JUN-2001; 2001US-0297414P.

12-JUN-2001; 2001US-0295573P.

12-JUN-2001; 2001US-0297567P.

14-JUN-2001; 2001US-0298285P.

14-JUN-2001; 2001US-0298285P.

18-JUN-2001; 2001US-0299133P.

19-JUN-2001; 2001US-0299230P.

21-JUN-2001; 2001US-0299494P.

22-JUN-2001; 2001US-0300177P.

26-JUN-2001; 2001US-0300883P.

28-JUN-2001; 2001US-0301530P.

28-JUN-2001; 2001US-0301550P.

03-JUL-2001; 2001US-0302951P.

31-JUL-2001; 2001US-0308890P.

14-SEP-2001; 2001US-0322297P.

25-SEP-2001; 2001US-0324669P.

03-DEC-2001; 2001US-0337477P.

14-DEC-2001; 2001US-0341562P.

21-FEB-2002; 2002US-0358656P.

21-FEB-2002; 2002US-0359112P.

22-FEB-2002; 2002US-0358978P.

22-FEB-2002; 2002US-0359034P.

22-FEB-2002; 2002US-0359035P.

22-FEB-2002; 2002US-0359121P.

27-FEB-2002; 2002US-0359646P.

01-MAR-2002; 2002US-0360858P.

12-MAR-2002; 2002US-0363430P.

13-MAR-2002; 2002US-0363767P.

10-APR-2002; 2002US-0371346P.

10-MAY-2002; 2002US-0379444P.

04-JUN-2002; 2002US-00379444.

(CURA-) CURAGEN CORP.

Agce ML, Anderson DW, Berghs C, Casman SU, Catterton E; Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA; Gerlach VL, Gorman L, Guo X, Herrmann JL, Hjal T, Ji W, Kekuda R; Khramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I; Ort T, Padigaru M, Patturajan M, Pena CE, Rastelli L, Rieger DK; Rothenberg ME, Shenoy SG, Shukets RA, Smithson G, Spaderna SK, Spyttek KA, Stone DJ, Vernet CM, Zhong H, Zhong M, Aisobrook JP; Burgess CE, Lepley DM;

WPI; 2003-210149/20.

P-PSDB; ADC10110.

New isolated NOVX polypeptides and nucleic acid molecules useful for treating, preventing and diagnosing pathological conditions with NOVX-associated disorders, such as cancer, obesity, diabetes and inflammatory or CNS diseases.

Claim 20; SEQ ID NO 129; 772pp; English.



QY 805 CCGAGGGTGTCTGCTCGGCTGTGGGAGTGGGAAAAGTCTGAGCGCCGCTCTCTG 864  
Db 878 CCGAGGGTGTCTGCTCGGCTGTGGGAGTGGGAAAAGTCTGAGCGCCGCTCTCTG 937  
QY 865 GCCAGAAATACAGGCTTGTCAATGCTGTGTGGCACTGCTGAAAGAGGCTGTGGCA 924  
Db 938 GCCAGAAATACAGGCTTGTCAATGCTGTGTGGCACTGCTGAAAGAGGCTGTGGCA 997  
QY 925 GATAGGACCAAGTGTGGGAGCTCATCCAGCCCTCTTTTGAAGAGAGTGGCAGTTCT 984  
Db 998 GATAGGACCAAGTGTGGGAGCTCATCCAGCCCTCTTTTGAAGAGAGTGGCAGTTCT 1057  
QY 985 GACAGCTCTCATGAAGTGTCTGAGCCAGGCTTGGACAGCAGGACTGCATCCAGAAA 1044  
Db 1058 GACAGCTCTCATGAAGTGTCTGAGCCAGGCTTGGACAGCAGGACTGCATCCAGAAA 1117  
QY 1045 GGCTGGGTGTCTACAGCGGCTCCCGCGGACTCTGACAGGCAACCTGTCTGAACCGCTG 1104  
Db 1118 GGCTGGGTGTCTACAGCGGCTCCCGCGGACTCTGACAGGCAACCTGTCTGAACCGCTG 1177  
QY 1105 GGCTACAAATCCAAACAGGCTTTTCTGAAATGTGCAATTTGATTCATCATGAGCGG 1164  
Db 1178 GGCTACAAATCCAAACAGGCTTTTCTGAAATGTGCAATTTGATTCATCATGAGCGG 1237  
QY 1165 CTGACTCTGAGAAGATTTGATCCAGTCACTGGGAAAGGTACCACTCATGTACAGCCA 1224  
Db 1238 CTGACTCTGAGAAGATTTGATCCAGTCACTGGGAAAGGTACCACTCATGTACAGCCA 1297  
QY 1225 CTTCCCACTGAGAGATCCAGGCTCGCTCTCTGAGAACCCAAAGATGCTGAAGCAG 1284  
Db 1298 CTTCCCACTGAGAGATCCAGGCTCGCTCTCTGAGAACCCAAAGATGCTGAAGCAG 1357  
QY 1285 GTCAAGCTGAAATGGAACCTTCTACAGAACTCAGCTGACTTGGAGCAGTTCTATGGG 1344  
Db 1358 GTCAAGCTGAAATGGAACCTTCTACAGAACTCAGCTGACTTGGAGCAGTTCTATGGG 1417  
QY 1345 TCGGCGCATCACCTCAATGGGACCCAGGACCCATACACAGTCTTCGAATACATCGAGT 1404  
Db 1418 TCGGCGCATCACCTCAATGGGACCCAGGACCCATACACAGTCTTCGAATACATCGAGT 1477  
QY 1405 GGGATCATTAATCCCTGCGCCCAAGAAATCCCTGA 1440  
Db 1478 GGGATCATTAATCCCTGCGCCCAAGAAATCCCTGA 1513

RESULT 5  
ADB63503  
ID ADB63503 standard; cDNA; 1619 BP.  
XX ADB63503;  
AC ADB63503;  
XX 04-DEC-2003 (first entry)  
DT Human cDNA encoding clone TBS2120244460.  
DE Human; ss; gene; pharmaceutical; diagnostic; gene therapy;  
XX tissue regeneration; cell regeneration; membrane protein;  
KW signal transduction-related protein; transcription-related protein;  
KW osteoporosis; neurological disease; cancer; tumour.  
XX Homo sapiens.  
OS  
XX Key Location/Qualifiers  
FH 684..1511  
FT /\*tag= a  
FT /product= "Clone TBS2120244460 protein"  
XX EP1308459-A2.  
XX 07-MAY-2003.  
XX 28-MAR-2002; 2002EP-00007401.  
PF

XX 05-NOV-2001; 2001JP-00379298.  
PR 25-JAN-2002; 2002US-00350978.  
XX (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX Isoqai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S,  
PI Yamamoto J, Isono Y, Otsuka K, Nagai K, Irie R, Tamechika I,  
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;  
XX WPI; 2003-450961/43.  
DR P-PSDB; ADB65473.  
XX New polynucleotides and polypeptides, useful for developing a diagnostic  
marker or medicines for regulation of their expression and activity, or  
as targets of gene therapy.  
XX Claim 1; Page; 22pp; English.  
XX The invention discloses a polynucleotide comprising a sequence selected  
from 1970 fully defined nucleotide sequences which encode novel  
polypeptides. Also claimed is a polypeptide encoded by the polynucleotide  
or its partial peptide, an antibody binding to the polypeptide or  
of the polynucleotide, immunologically assaying the polypeptide or  
peptide of the polynucleotide by contacting the polypeptide or peptide  
with the antibody of the encoded protein, and observing the binding  
between the two, a transformant carrying the polynucleotide in an  
expressible manner and an antisense polynucleotide, or as a probe  
for detecting the polynucleotide. The polynucleotides and encoded  
proteins are useful as pharmaceutical agents and many disease-related  
genes may be included in them, for developing a diagnostic marker or  
medicines for regulation of their expression and activity, or as targets  
of gene therapy. The genes are involved in tissue and/or cell  
regeneration. Membrane proteins, signal transduction-related proteins,  
transcription-related proteins, disease-related proteins and genes  
encoding them can be used as indicators for diseases (e.g. osteoporosis,  
neurological diseases, cancer, tumours). The cDNA may be used to regulate  
the activity or expression of the encoded protein to treat diseases. The  
sequence presented is a cDNA of the invention. Note: Some of the sequence  
data for this patent is not represented in the printed specification, but  
is based on sequence information supplied by the European Patent Office.  
XX Sequence 1619 BP; 397 A; 469 C; 425 G; 328 T; 0 U; 0 Other;  
SQ

Query Match 81.2%; Score 1170; DB 10; Length 1619;  
Best Local Similarity 93.3%; Pred. No. 1.4e-294;  
Matches 1272; Conservative 0; Mismatches 0; Indels 92; Gaps 1;  
QY 169 GTGCCAGGATTGTAATATTAGTCCACCCGCTCAGGGAAAACAAATAGCAATGTGG 228  
Db 148 GTGCCAGGATTGTAATATTAGTCCACCCGCTCAGGGAAAACAAATAGCAATGTGG 207  
QY 229 CTCTGCAAAATCTGAACAGCAGTCTCTCACCTGGAGAACCTGATCTTAATGAGTTT 288  
Db 208 CTCTGCAAAATCTGAACAGCAGTCTCTCACCTGGAGAACCTGATCTTAATGAGTTT 267  
QY 289 TCCTATACGGCCACCGAGGCAAGGCTTTATCTGCAAGGAGACAGTCTCCAGCGCG 348  
Db 268 TCCTATACGGCCACCGAGGCAAGGCTTTATCTGCAAGGAGACAGTCTCCAGCGCG 327  
QY 349 CTGCTCGTCCAGCTGATTCAGGAACCGCTCGCTGAGAGATTCATCAAGCAGTTT 402  
Db 328 CTGCTCGTCCAGCTGATTCAGGAACCGCTCGCTGAGAGATTCATCAAGCAGTTT 387  
QY 403 ----- 402  
Db 388 GTTTCCTGTAATAGCCGCTTTCGAGTTTTCATCGGTAATTCAGTATCTGAGTTACGTG 447  
QY 403 -----GGCTGGATTCCTGGATGGCATCCCTGAGACCGGTG 436  
Db 448 GTGGTGACATCTGTATCTGCTCTCATGCTGGATTCCTGGATGGCATCCCTGAGACCGGTG 507





PT treating, preventing and diagnosing pathological conditions with NOVX-  
PT associated disorders, such as cancer, obesity, diabetes and inflammatory  
PT or CNS diseases.

PS Claim 20; SEQ ID NO 127; 772pp; English.

XX The invention relates to novel isolated polypeptides, mature form of the  
CC polypeptide, a sequence that is 95% identical to the polypeptide or the  
CC polypeptide comprising one or more conservative substitutions. The NOVX  
CC polypeptide is useful for treating or preventing a pathology associated  
CC with the polypeptide e.g. disorders associated with aberrant expression  
CC or activity of the polypeptide, such as cancer, diabetes, obesity, and  
CC endocrine, CNS and inflammatory disorders. They can also be used in  
CC various detection and screening assays, chromosome mapping, tissue typing  
CC and predictive medicine. This sequence corresponds to the coding sequence  
CC for one of the polypeptides of the invention.

XX SQ Sequence 1967 BP; 461 A; 594 C; 555 G; 357 T; 0 U; 0 Other;

Query Match 81.0%; Score 1166; DB 10; Length 1967;  
Best Local Similarity 90.8%; Pred. No. 1.7e-293;  
Matches 1308; Conservative 0; Mismatches 0; Indels 132; Gaps 1;

QY 1 ATGACGCCACTATCGCCCGCAGCGTATCCCCCGCAGATGCCCCAGTAGCGGGAGGAG 60  
DB 552 ATGACGCCACTATCGCCCGCAGCGTATCCCCCGCAGATGCCCCAGTAGCGGGAGGAG 611  
QY 61 AACCACTCTTCAGTTCATGAGCAATGTCGAGCAATCTCTGATCCACCGCCGAA 120  
DB 612 AACCACTCTTCAGTTCATGAGCAATGTCGAGCAATCTCTGATCCACCGCCGAA 671  
QY 121 GATCCATCCCTTCATGATCCAGCACTTGCATAGAGCAACAGCAATGTGCCAGGATT 180  
DB 672 GATCCATCCCTTCATGATCCAGCACTTGCATAGAGCAACAGCAATGTGCCAGGATT 731  
QY 181 GTAATATTAGTTCACCGCCCTCAGGAAAACAATAGCAATGTGGCTCTGCAACAT 240  
DB 732 GTAATATTAGTTCACCGCCCTCAGGAAAACAATAGCAATGTGGCTCTGCAACAT 791  
QY 241 CTGACACGAGCTCTCTACCCCTGAGAACCTGATCTTAATGATTTTCTATACGCCC 300  
DB 792 CTGACACGAGCTCTCTACCCCTGAGAACCTGATCTTAATGATTTTCTATACGCCC 851  
QY 301 ACCGAGCCAGAGGCTTTATCTGCAAGGAAGACAGTTCCAGCGCCTGCTGTCAG 360  
DB 852 ACCGAGCCAGAGGCTTTATCTGCAAGGAAGACAGTTCCAGCGCCTGCTGTCAG 911  
QY 361 CTGATTCAGAACGCTGCTGAGAGGATTCATCAGAGGCTGATTTCTGATGGC 420  
DB 912 CTGATTCAGAACGCTGCTGAGAGGATTCATCAGAGGCTGATTTCTGATGGC 971  
QY 421 ATCCCTGAGACGCTGAGAGGCTCTGAGGATCCAGACCTGGGATCACACCCAGAC 480  
DB 972 ATCCCTGAGACGCTGAGAGGCTCTGAGGATCCAGACCTGGGATCACACCCAGAC 1031  
QY 481 GTCAATGTGAGTCTCAGACAGCTGCTGATCGAGAACTTGGGAGAGATC 540  
DB 1032 GTCAATGTGAGTCTCAGACAGCTGCTGATCGAGAACTTGGGAGAGATC 1091  
QY 541 GACCCCTCAACTCGAGAGATTTATCACACACCTTTGATGGCCACCCGAAATCTGAAATC 600  
DB 1092 GACCCCTCAACTCGAGAGATTTATCACACACCTTTGATGGCCACCCGAAATCTGAAATC 1151  
QY 601 CAGAACCGTCTCATGTGTCAGAGGACATCTCAGAGCTGAGACGGCTCAGAACTGCTG 660  
DB 1152 CAGAACCGTCTCATGTGTCAGAGGACATCTCAGAGCTGAGACGGCTCAGAACTGCTG 1211  
QY 661 GAGTATCATAGGAACATCTGAGGCTCATTTCCCTTACCCCAAAATCTCAAAGTCATC 720  
DB 1212 GAGTATCATAGGAACATCTGAGGCTCATTTCCCTTACCCCAAAATCTCAAAGTCATC 1271  
QY 721 AGTGCTCAGCAGGCAATGTGTGGAGCTTCTTACAGGCTCTGACCTATGTCTCAAAGCAAC 780

DB 1272 AGTGCTCAGCAGGCAATGTGTGGAGCTTCTTACAGGCTCTGACCTATGTCCAAAGCAAC 1331  
QY 781 CATCGTACTAATGCCCCGTTTACCCCCGAGGGTGTCTGTCTCGGGCCTGTGGGAGTGGG 840  
DB 1332 CATCGTACTAATGCCCCGTTTACCCCCGAGGGTGTCTGTCTCGGGCCTGTGGGAGTGGG 1391  
QY 841 AAAAGTCTGAGGGCGCCCTCTGCGCCAGAAATACAGGCTTGTCAATGTCTGTCTGGG 900  
DB 1392 AAAAGTCTGAGGGCGCCCTCTGCGCCAGAAATACAGGCTTGTCAATGTCTGTCTGGG 1451  
QY 901 CAACCTGCTGAAAGAGGCTGTGCGCAGATAGGACACAGTTTGGCGAGCTCATCCAGCCCTTC 960  
DB 1452 CAACCTG----- 1457  
QY 961 TTTGAAAAGAGAGTGGCAGTTCTCTGACAGCCCTCTCATGAAGTGTGTGAGCCAGGCGCTG 1020  
DB 1458 ----- 1457  
QY 1021 GACCAGCAGGACTGATCCAGAAAGGCTGGGTGTCTACACGGCGTCCCGGGGACCTCGAC 1080  
DB 1458 -----CAGAAAGGCTGGGTGTCTACACGGCGTCCCGGGGACCTCGAC 1499  
QY 1081 CAGGCACACCTCTGTAACCGCTGGGCTACAATCCAAACAGGGTGTCTTCTCTGAATGTG 1140  
DB 1500 CAGGCACACCTCTGTAACCGCTGGGCTACAATCCAAACAGGGTGTCTTCTCTGAATGTG 1559  
QY 1141 CAATTGTATTCATCATGAGGCGGCTGACTCTGAGAGAAATGTGATCTCACTGAGGAA 1200  
DB 1560 CAATTGTATTCATCATGAGGCGGCTGACTCTGAGAGAAATGTGATCTCACTGAGGAA 1619  
QY 1201 AGGTACCACTCATGTACAAAGCCACTCCCACTGAGAGATCCAGGCTCGCTCTGAG 1260  
DB 1620 AGGTACCACTCATGTACAAAGCCACTCCCACTGAGAGATCCAGGCTCGCTCTGAG 1679  
QY 1261 AACCCAAAGGATGCTGAAAGAGCAGGTCAAGCTGAAAATGGAACCTTTCTACAGGAATCA 1320  
DB 1680 AACCCAAAGGATGCTGAAAGAGCAGGTCAAGCTGAAAATGGAACCTTTCTACAGGAATCA 1739  
QY 1321 GCTGACTCTGAGCAGTGTGATGCTGGGCACTACCCCTCAATGGGGACACAGACCCATAC 1380  
DB 1740 GCTGACTCTGAGCAGTGTGATGCTGGGCACTACCCCTCAATGGGGACACAGACCCATAC 1799  
QY 1381 ACAGTCTTCTGAAATACATCGAGAGTGGATCATTAATCCCTGCCCCAGAAAATCCCTGA 1440  
DB 1800 ACAGTCTTCTGAAATACATCGAGAGTGGATCATTAATCCCTGCCCCAGAAAATCCCTGA 1859

RESULT 7  
AADI4324  
ID AADI4324 standard; cdna; 1452 BP.

XX AC AADI4324;

XX AC AADI4324;

DT 01-NOV-2001 (first entry)

XX Human 27802 adenylate kinase cdna.

Human; 27802 protein; adenylate kinase; cellular proliferative disorder;  
neurological disorder; inflammatory disorder; lymphatic disorder;  
cardiovascular disorder; respiratory disorder; haematological disorder;  
Crohn's disease; atherosclerosis; pernicious anaemia; asthma; leukaemia;  
acquired immune deficiency syndrome; AIDS; multiple sclerosis; lymphoma;  
Alzheimer's disease; systemic lupus erythematosus; SLE; gene therapy;  
lymphoblastic leukaemia; T-cell neoplasm; cytostatic; neuroprotective;  
tissue typing; antileukosclerotic; chromosomal mapping; nontropic;  
dermatological; antiinflammatory; immunosuppressive; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS 219..995

XX FT /\*tag= a

XX FT /product= "Human 27802 adenylate kinase"

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FT misc_feature 219..992
FT /tag= b
FT /note= "This region is specifically referred in claim 2"
FT sig_peptide 219..386
FT /tag= b
FT mat_peptide 387..992
FT /tag= c
FT /product= "Human mature 27802 adenylate kinase"
XX W0200159082-A1.
XX
XX 16-AUG-2001.
XX
XX 12-FEB-2001; 2001WO-US004573.
XX
XX 10-FEB-2000; 2000US-0181705P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Kapeller-Libermann R, Chun M;
XX
XX WPI; 2001-514661/56.
XX
XX P-PSDB; AAE07843.
XX
XX New adenylate kinase polypeptide for diagnosing/treating cellular
XX proliferative and/or differentiative, neurological, immune, inflammatory,
XX lymphatic, cardiovascular, respiratory and hematological disorders.
XX
XX Claim 2; Fig 1; 108pp; English.
XX
XX The present sequence is a cDNA encoding human 27802 adenylate kinase. The
XX 27802 protein and its corresponding nucleotide sequence is useful for
XX modulating, diagnosing and treating cellular proliferative and/or
XX differentiative, neurological, inflammatory, lymphatic, cardiovascular,
XX immune, respiratory and hematological disorders. 27802 sequence is
XX useful for treating immune disorders (e.g., Crohn's disease), disorders
XX involving blood vessels (e.g., atherosclerosis), disorders involving red
XX cells (e.g., pernicious anemia), respiratory disorders (e.g., asthma),
XX disorders involving brain and lymph nodes (e.g., acquired immune
XX deficiency syndrome (AIDS), multiple sclerosis, Alzheimer's disease),
XX disorders involving T-cells (e.g., systemic lupus erythematosus),
XX diseases involving haematopoietic stem cells (e.g., leukaemia), disorders
XX involving B-cells (e.g., lymphoblastic leukaemia/lymphoma) and disorders
XX modulating precursor T-cell neoplasms. 27802 sequence is useful for
XX particularly for regulating one or more proteins involved in growth and
XX metabolism. 27802 DNA is used in gene therapy. 27802 sequence or its
XX antibody are useful in screening assays, detection assays (e.g.,
XX chromosomal mapping, tissue typing, forensic biology), preventive
XX medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical
XX trials and pharmacogenomics) and in methods of treatment
XX
XX Sequence 1452 BP; 398 A; 414 C; 364 G; 276 T; 0 U; 0 Other;
XX
XX Query Match 71.7%; Score 1032.8; DB 4; Length 1452;
XX Best Local Similarity 86.5%; Pred. No. 8.3e-259;
XX Matches 1246; Conservative 0; Mismatches 2; Indels 192; Gaps 2;
XX
XX 1 ATGAGCGCCACTATGCGCCGACCGTATCCCGCCGAGATGCCAGTACCGGGAGGAG 60
XX 53 ATGAGCGCCACTATGCGCCGACCGTATCCCGCCGAGATGCCAGTACCGGGAGGAG 112
XX
XX 61 AACACATCTTCGAGTTGATGCGAACATGCTGAGGACATCTCTGATCCACAGCCCGAA 120
XX 113 AACACATCTTCGAGTTGATGCGAACATGCTGAGGACATCTCTGATCCACAGCCCGAA 172
XX
XX 121 GATCCCATCCCTTCATGATCCAGCACTTGTCATAGAGAACACCAATGTGCCAGGATT 180
XX 173 GATCCCATCCCTTCATGATCCAGCACTTGTCATAGAGAACACCAATGTGCCAGGATT 221
XX
XX 181 GTAATATTAGTCTCCACCGCTTCAGGAAACCAATAGCAATGTGCTTCGAAACAT 240
XX 222 -----GCATGTGGCTCTGCACCAT 242
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Qy 241 CTGAACAGCAGCTCTCTCACTCCCTGGAGAACCTGATCTTAAATGAGTTTTCTATACGGCC 300
Db 243 CTGAACAGCAGCTCTCTCACTCCCTGGAGAACCTGATCTTAAATGAGTTTTCTATACGGCC 302
Qy 301 ACCGAAGCCAGAGGCTTTATCTGCAAAAGAGAGACAGTTCCAGCGGCTGCTCGTCCAG 360
Db 303 ACCGAAGCCAGAGGCTTTATCTGCAAAAGAGAGACAGTTCCAGCTGCTCGTCCAG 362
Qy 361 CTGATTTCAGGAACCGCTTGGCTGAAGAGGATTCATCAAGCAGGGCTGATCTTGGATGGC 420
Db 363 CTGATTTCAGGAACCGCTTGGCTGAAGAGGATTCATCAAGCAGGGCTGATCTTGGATGGC 422
Qy 421 ATCCCTGAGACCGCTGAGCAGGCTCTGAGGATCCAGACCTTGGGGATCAACCCAGACAC 480
Db 423 ATCCCTGAGACCGCTGAGCAGGCTCTGAGGATCCAGACCTTGGGGATCAACCCAGACAC 482
Qy 481 GTCAATTGTGCTGCTCCAGACACGCTCTGATCGAGAGAAACTTTGGGGAAGAGAAATC 540
Db 483 GTCAATTGTGCTGCTCCAGACACGCTCTGATCGAGAGAAACTTTGGGGAAGAGAAATC 542
Qy 541 GACCCCTCAAACTGGAGAGATTTATCAACCACTTTGACTGGCCACCCGGAATCTGAAATC 600
Db 543 GACCCCTCAAACTGGAGAGATTTATCAACCACTTTGACTGGCCACCCGGAATCTGAAATC 602
Qy 601 CAGAACGCTCTCATGCTGGCCAGAGGACATCTCAGAGCTGGAGAGCGCTCAGAACTGCTG 660
Db 603 CAGAACGCTCTCATGCTGGCCAGAGGACATCTCAGAGCTGGAGAGCGCTCAGAACTGCTG 662
Qy 661 GAGTATCATAGGAACAATGTCAGGCTCAATTCCTCTCAACCCAAATCTCTCAAGTCAATC 720
Db 663 GAGTATCATAGGAACAATGTCAGGCTCAATTCCTCTCAACCCAAATCTCTCAAGTCAATC 722
Qy 721 AGTGTGACACGACCATGTGTGGACGCTCTTACACAGGCTCTGACCTATGTCTCAAGACCA 780
Db 723 AGTGTGACACGACCATGTGTGGACGCTCTTACACAGGCTCTGACCTATGTCTCAAGACCA 782
Qy 781 CATGCTACTTAATCCCGCTTACCCGAGGCTGCTGCTCGGGCTGCTGGGCGATGGG 840
Db 783 CATGCTACTTAATCCCGCTTACCCGAGGCTGCTGCTCGGGCTGCTGGGCGATGGG 842
Qy 841 AAAAGTCTGACGCGCCCTCTCTGCGCCAGAAATAAGGCTTGTCAATGTCTGTGTTGGG 900
Db 843 AAAAGTCTGACGCGCCCTCTCTGCGCCAGAAATAAGGCTTGTCAATGTCTGTGTTGGG 902
Qy 901 CAATGCTGAAAGAGGCTGTGCGACATAGGACACAGCTTTGGCGAGCTCATCCAGCCCTTC 960
Db 903 CAATGCTGAAAGAGGCTGTGCGACATAGGACACAGCTTTGGCGAGCTCATCCAGCCCTTC 962
Qy 961 TTTGAAAGAGGATGTCAGTTCCTGACAGCTCTCTCATGAAGTGTGTGAGCCAGCGCTG 1020
Db 963 TTTGAAAGAGGATGTCAGTTCCTGACAGCTCTCTCATGAAGTGTGTGAGCCAGCGCTG 978
Qy 1021 GACCAGCAGGACTGCTCATCAGAAAGCTGGGTGTCTACACGGCTCCCGGGGACCTCGAC 1080
Db 979 ----- 978
Qy 1081 CAGGCACACCTGCTGAAACCGCTGGGCTCAATCCCAACAGGCTGTTTTTCTGTAATGTG 1140
Db 979 -----CAGGCTGTTTTTCTGTAATGTG 1000
Qy 1141 CCATTTGATTTCCATCATGAGCGGCTGACTCTGAGAGAAATTTGATCAGTCACTCGGGAA 1200
Db 1001 CCATTTGATTTCCATCATGAGCGGCTGACTCTGAGAGAAATTTGATCAGTCACTCGGGAA 1060
Qy 1201 AGGTACCACTCATGTACAGCCACCTCCACCATGAGATCCAGGCTCGCTCTCTCGAG 1260
Db 1061 AGGTACCACTCATGTACAGCCACCTCCACCATGAGATCCAGGCTCGCTCTCTCGAG 1120
Qy 1261 AACCCAAAGGATGCTGAGAGAGCGTCAAGCTGAAATGGAATCTGTTCTTACAGGAATCA 1320
Db 1121 AACCCAAAGGATGCTGAGAGAGCGTCAAGCTGAAATGGAATCTGTTCTTACAGGAATCA 1180
```





PR	25-SEP-2000;	2000US-0234988P.	XX	PA	(HUMA-) HUMAN GENOME SCI INC.
PR	26-SEP-2000;	2000US-0235484P.	XX	PI	Rosen CA, Barash SC, Ruben SM;
PR	27-SEP-2000;	2000US-0235834P.	XX	XX	WPI; 2001-465460/50.
PR	29-SEP-2000;	2000US-0236327P.	DR	DR	P-PSDB; AAU17305.
PR	29-SEP-2000;	2000US-0236367P.	XX	XX	Novel polypeptides useful for diagnosing, treating, preventing and/or
PR	29-SEP-2000;	2000US-0236368P.	PT	PT	prognosing disorders related to the proteins, including cancers, immune
PR	29-SEP-2000;	2000US-0236369P.	PT	PT	disorders and neuronal disorders.
PR	29-SEP-2000;	2000US-0236370P.	XX	XX	Claim 1; SEQ ID NO 257; 880pp; English.
PR	02-OCT-2000;	2000US-0236802P.	PS	PS	The invention relates to novel isolated polypeptides (I), and
PR	02-OCT-2000;	2000US-0237037P.	XX	XX	polynucleotides (II). (I), (II) and the antibody to (I) are useful for
PR	02-OCT-2000;	2000US-0237039P.	CC	CC	diagnosing, preventing and treating diseases including immune system
PR	13-OCT-2000;	2000US-0239935P.	CC	CC	disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
PR	13-OCT-2000;	2000US-0239937P.	CC	CC	disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
PR	20-OCT-2000;	2000US-0240960P.	CC	CC	transplant rejections and graft versus host disease, infectious diseases
PR	20-OCT-2000;	2000US-0241221P.	CC	CC	(e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
PR	20-OCT-2000;	2000US-0241785P.	CC	CC	other blood-related disorders (sickle cell anaemia), myeloproliferative
PR	20-OCT-2000;	2000US-0241786P.	CC	CC	disorders, primary haematopoietic disorders, hyperproliferative disorders
PR	20-OCT-2000;	2000US-0241808P.	CC	CC	(e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.
PR	20-OCT-2000;	2000US-0241809P.	CC	CC	Alzheimer's disease, Parkinson's disease), chromosomal abnormalities
PR	01-NOV-2000;	2000US-0244617P.	CC	CC	(Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.
PR	08-NOV-2000;	2000US-0246474P.	CC	CC	glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),
PR	08-NOV-2000;	2000US-0246475P.	CC	CC	respiratory disorders, dermatological disorders, in wound healing,
PR	08-NOV-2000;	2000US-0246476P.	CC	CC	epithelial cell proliferation, endocrine disorders (e.g. Addison's
PR	08-NOV-2000;	2000US-0246477P.	CC	CC	disease), reproductive system disorders, gastrointestinal disorder
PR	08-NOV-2000;	2000US-0246478P.	CC	CC	(inflammatory disorders), liver disorders (cirrhosis), as stimulators of
PR	08-NOV-2000;	2000US-0246522P.	CC	CC	B-cell responsiveness to pathogens, activators of T-cells, to induce
PR	08-NOV-2000;	2000US-0246524P.	CC	CC	higher affinity antibodies, and as a means to induce tumour proliferation
PR	08-NOV-2000;	2000US-0246525P.	CC	CC	in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAS26976-
PR	08-NOV-2000;	2000US-0246526P.	CC	CC	AAS27850 represent novel signal transduction pathway protein coding
PR	08-NOV-2000;	2000US-0246527P.	XX	XX	sequences and PCR primers of the invention
PR	08-NOV-2000;	2000US-0246528P.	XX	XX	
PR	08-NOV-2000;	2000US-0246529P.	XX	XX	
PR	08-NOV-2000;	2000US-0246609P.	XX	XX	
PR	08-NOV-2000;	2000US-0246610P.	XX	XX	
PR	08-NOV-2000;	2000US-0246611P.	XX	XX	
PR	08-NOV-2000;	2000US-0246612P.	XX	XX	
PR	08-NOV-2000;	2000US-0246613P.	XX	XX	
PR	17-NOV-2000;	2000US-0249207P.	QY	QY	1 ATGGAGCCCACTATCGCCCGCACCGCATATCCCGCCGAGATCCCGAGTACCGGGAGGAG 60
PR	17-NOV-2000;	2000US-0249208P.	Db	Db	6 ATGAGCGCCACTATCGCCCGCACCGCATATCCCGCCGAGATCCCGAGTACCGGGAGGAG 63
PR	17-NOV-2000;	2000US-0249209P.	QY	QY	61 AACCACTCTTCGAGTTGATG-----CAG 84
PR	17-NOV-2000;	2000US-0249211P.	Db	Db	64 AACCACTCTTCGAGTTGATG-----CAG 84
PR	17-NOV-2000;	2000US-0249212P.	QY	QY	85 AACATGCTGGAGCAACTCTCTGATCCACCGCCGAGATCCCATCCCTTCATGATCCAG 144
PR	17-NOV-2000;	2000US-0249215P.	Db	Db	124 AACATGCTGGAGCAACTCTCTGATCCACCGCCGAGATCCCATCCCTTCATGATCCAG 183
PR	17-NOV-2000;	2000US-0249217P.	QY	QY	145 CACTTGCATAGACAAACGCAATGTCGCGAGATGTAATATAGTCCACCGGCTCA 204
PR	17-NOV-2000;	2000US-0249218P.	Db	Db	184 CACTTGCATAGACAAACGCAATGTCGCGAGATGTAATATAGTCCACCGGCTCA 243
PR	17-NOV-2000;	2000US-0249244P.	QY	QY	205 GGGAAACCAATAGCAATGTCGCTCTGCAACATCTG-AAACAGAGTCTCTCCACCCCT 263
PR	17-NOV-2000;	2000US-0249245P.	Db	Db	244 GGGAAACCAATAGCAATGTCGCTCTGCAACATCTGAAACAGAGTCTCTCCACCCCT 303
PR	17-NOV-2000;	2000US-0249265P.	QY	QY	264 GGA-GAACCTGATCTTAAATGAGTTTCTTATACGGCCACCGAGCCAG-AAGGCTTTAT 321
PR	01-DEC-2000;	2000US-0250391P.	Db	Db	304 GGANGAACCTGATCTTAAATGAGTTTCTTATACGGCCACCGAGCCAGAAAGGCTTTAT 363
PR	05-DEC-2000;	2000US-0251030P.	QY	QY	322 CTGCAAAAGGAAGACAGTTCCAGCGGCTGCTCGTCAGCTGATTTCAGGAACCGCTGGCT 381
PR	05-DEC-2000;	2000US-0251988P.	Db	Db	364 CTGCAAAAGGAAGACAGTTCCAGCGGCTGCTCGTCAGCTGATTTCAGGAACCGCTGGCT 423
PR	06-DEC-2000;	2000US-0251479P.	QY	QY	382 GAAGAGGATTGCATCAAGCAGCGGCTGGAATCTGAGTGGCATCTCTGAGACGCGTGAGCAG 441
PR	08-DEC-2000;	2000US-0251868P.	Db	Db	424 GAAGAGGATTGCATCAAGCAGCGGCTGGAATCTGAGTGGCATCTCTGAGACGCGTGGA-CAG 482
PR	08-DEC-2000;	2000US-0251869P.			
PR	08-DEC-2000;	2000US-0251989P.			
PR	08-DEC-2000;	2000US-0251990P.			
PR	11-DEC-2000;	2000US-0254097P.			
PR	05-JAN-2001;	2001US-0259678P.			



QY 442 GCTCTGAGGATCCAGACCTCGGGATCACCACAGCATCTGCTGAGTGTCCA 501  
Db 483 GCTCTGAGGATCCAGACCTCGGGATCACCACAGCATCTGCTGAGTGTCCA 542  
QY 502 GACACGGTCTCTGATCGAGAGAACTTGGGGAAGAGATCGACCTCAAACTGGAGAGATT 561  
Db 543 GACACGGTCTCTGATCGAGAGAACTTGGGGAAGAGATCGACCTCAAACTGGAGAGATT 602  
QY 562 TATCACACACCTTTGATCTGCGCCACCCGAATCTGAAATCCAGAACCGTCTCATGGTGCCA 621  
Db 603 TATCACACACCTTTGATCTGCGCCACCCGAATCTGAAATCCAGAACCGTCTCATGGTGCCA 662  
QY 622 GAGGACATCTCAGAGCTGGAGCGGCTCAGAACTCTGGAGTATCATAGAACATCGTC 681  
Db 663 GAGGACATCTCAGAGCTGGAGCGGCTCAGAACTCTGGAGTATCATAGAACATCGTC 722  
QY 682 AGGGTCATTCTCTCTACCCCAAAATCTCAAGTCATCAGTGTGACCGCATCTGTG 741  
Db 723 AGGGTCATTCTCTCTACCCCAAAATCTCAAGTCATCAGTGTGACCGCATCTGTG 782  
QY 742 GAGCTCTTCTACCGGCTCTGACCTATGTCCAAAGAACCATCTGTAATGCCCGTTC 801  
Db 783 GAGCTCTTCTACCGGCTCTGACCTATGTCCAAAGAACCATCTGTAATGCCCGTTC 842  
QY 802 ACCCGAGGGTGTCTGTCTCGGCTTGTGGGAGTGGGAAAAAGTCTGCAGGCGCGCCCTC 861  
Db 843 ACCCGAGGGTGTCTGTCTCGGCTTGTGGGAGTGGGAAAAAGTCTGCAGGCGCGCCCTC 902  
QY 862 CTGGCCCAAGAAATACAGCTTGTCAATGTCTGCTGGGCAACTCTGAAAGAGGCTGTG 921  
Db 903 CTGGCCCAAGAAATACAGCTTGTCAATGTCTGCTGGGCAACTCTGAAAGAGGCTGTG 962  
QY 922 GCAGATAGGACCGAGTTTGGGAGCTCATCGACCTTCTTTGAAAAGAGATGCGAGTT 981  
Db 963 GCAGATAGGACCGAGTTTGGGAGCTCATCGACCTTCTTTGAAAAGAGATGCGAGTT 1022  
QY 982 CTGACAGCTCTCTATGAAGGTGTGACCGACCGCTTGGACAGCAGCACTGCATCCAG 1041  
Db 1023 CTGACAGCTCTCTATGAAGGTGTGACCGACCGCTTGGACAGCAGCACTGCATCCAG 1082  
QY 1042 AAAGCTGGGTGTCTACACGGCTTCCCGGGAGCTTCCAGCAGGACACCTGCTGAACCGC 1101  
Db 1083 AAAGCTGGGTGTCTACACGGCTTCCCGGGAGCTTCCAGCAGGACACCTGCTGAACCGC 1142  
QY 1102 CTGGGTACAA-TCCCAACAGGTGTCTTCTGAAATGCTGCTGATTCATCATGA 1160  
Db 1143 CTGGGTACAA-TCCCAACAGGTGTCTTCTGAAATGCTGCTGATTCATCATGA 1202  
QY 1161 CGGGCT 1166  
Db 1203 NCGGT 1208

RESULT 10  
ADB93400

ID ADB93400 standard; cDNA; 1223 BP.

XX AC ADB93400;

XX DT 04-DEC-2003 (first entry)

XX DE Human cDNA encoding a novel protein #247.

XX KW ss; gene; human; autoimmune disease; Parkinson's disease; silicosis;  
XX KW gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia;  
XX KW immunosuppressive agent; adjuvant; enhance immune response;  
XX KW higher affinity antibody induction;  
XX KW increased serum immunoglobulin concentration.

OS Homo sapiens.

XX US2002168711-A1.

XX PD 14-NOV-2002.  
XX PF 17-JAN-2001; 2001US-00764868.  
XX 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217486P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 22-AUG-2000; 2000US-0226688P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 21-SEP-2000; 2000US-0231413P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 25-SEP-2000; 2000US-0234274P.  
PR 27-SEP-2000; 2000US-0234997P.  
PR 29-SEP-2000; 2000US-0235834P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 02-OCT-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 13-OCT-2000; 2000US-0237040P.  
PR 20-OCT-2000; 2000US-0239935P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 01-NOV-2000; 2000US-0241809P.  
PR 17-NOV-2000; 2000US-0244617P.  
PR 08-DEC-2000; 2000US-0249299P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
XX (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
XX (BARA/) BARASH S C.  
PI Rosen CA, Ruben SM, Barash SC;  
XX WPI; 2003-719985/68.  
DR P-PSDB; ADB94013.  
XX New isolated polypeptide useful for diagnosing and treating  
XX immunosuppressive conditions such as autoimmune disease and Parkinson's  
XX disease.  
PS Claim 3; SEQ ID NO 257; 345pp; English.  
XX The invention relates to an isolated polypeptide. The polypeptide is  
XX useful for diagnosing a pathological condition or a susceptibility to a

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pathological condition in a subject, by determining the presence or amount of expression of the polypeptide in a biological sample and diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide. The polypeptide is also useful for identifying a binding partner to the polypeptide, which involves contacting the polypeptide with a binding partner and determining whether the binding partner effects an activity of the polypeptide. The polypeptide or the nucleic acid encoding the polypeptide is useful for preventing, treating, or ameliorating a medical condition, which involves administering the polypeptide or the nucleic acid to a mammalian subject. The nucleic acid is useful for diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, which involves determining the presence or absence of a mutation in the nucleic acid, and diagnosing a pathological condition or susceptibility to a pathological condition based on the presence or absence of the mutation. The polypeptide, the nucleic acid and an antibody to the polypeptide are useful for treating autoimmune disease, Parkinson's disease, silicosis, gastrointestinal disease, atherosclerosis, haemophilia, thrombocytopenia. The polypeptide, the nucleic acid and the antibody are useful as immunosuppressive agents as adjuvants to enhance immune responses, and as agents to induce higher affinity antibodies and increase serum immunoglobulin concentrations. The present sequence represents cDNA encoding a novel human protein. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format direct from USPTO at [seqdata.uspto.gov/sequence.html?DocID=20020168711](http://seqdata.uspto.gov/sequence.html?DocID=20020168711).

XX  
50  
sequence 1223 BP: 305 A: 355 C: 310 G: 245 T: 0 U: 8 Other;

Query Match	71.4%;	Score 1027.6;	DB 10;	Length 1223;
Best Local Similarity	95.6%;	Prod. No. 1.8e-257;		
Matches 1153;	Conservative	0;	Mismatches 10;	Indels 43; Gaps 8;
QY	1	ATGGACGCCCATCTATCGCCCCCGCACCGTATCCCCCCCGAGATGCCCCAGTACGGGAGGAG	60	
DB	6	ATGGACGCCCATCTATCGCCCCCGCACCGTATCCCCCCCGAGA-GCCCCCAGTAC-GGGAGGAG	63	
QY	61	AACCCATCTTCGAGTTCATG-----CAG	84	
DB	64	AACCCATCTTCGGNNTGATGCAAGTATTAAACCACCTGGGTGTCGCCCTGCACCCACAG	123	
QY	85	AACATGCTGGAGCAACTCTCTGATCCACAGGCCCGGAAGATCCGATCCCTTCATGATCCAG	144	
DB	124	AACATGCTGGAGCAACTCTCTGATCCACAGGCCCGGAAGATCCGATCCCTTCATGATCCAG	183	
QY	145	CACTTTGCAATAGAGACAAACGACAAATGTGCCAGATTGTAAATATTAGTCCACCGCCCTCA	204	
DB	184	CACTTTGCAATAGAGACAAACGACAAATGTGCCAGATTGTAAATATTAGTCCACCGCCCTCA	243	
QY	205	GGGAAACAAACAATAGCAATGTGGCTCTGCAAAACATCTG-AACAGCAGTCTCCACCCCT	263	
DB	244	GGGAAACAAACAATAGCAATGTGGCTCTGCAAAACATCTGAAACAGCAGTCTCTCACCCCT	303	
QY	264	GGA-GAACCTGATCTTAAATAGATTTCCTATACCGCCACCGAAGCCAG-AAGGCTTTAT	321	
DB	304	GGANGAACCTGATCTTAAATAGATTTCCTATACCGCCACCGAAGCCAGAAAGGCTTTAT	363	
QY	322	CTGCAAGGAAGACAGATTCCGACGGCTGCTGCTCCAGTCAATTCAGGAACGCTGGCT	381	
DB	364	CTGCAAGGAAGACAGATTCCGACGGCTGCTGCTCCAGTCAATTCAGGAACGCTGGCT	423	
QY	382	GAAGAGGATTGCATCAAGCAGGCTGGATTCTGGATGGCATCCCTGAGACGCGTGAGCAG	441	
DB	424	GAAGAGGATTGCATCAAGCAGGCTGGATTCTGGATGGCATCCCTGAGACGCGTGAG-CAG	482	
QY	442	GCCTCAGGATCCAGACCCCTGGGGATCACACCAGACAGTCAATTGTGCTGAGTGTCTCA	501	
DB	483	GCCTCAGGATCCAGACCCCTGGGGATCACACCAGACAGTCAATTGTGCTGAGTGTCTCA	542	
QY	502	GACACGGTCTGATTCAGAGAAACTTTGGGGAAGAGAAATCGACCCCTCAAACTCGAGAGATT	561	
DB	543	GACACGGTCTGATTCAGAGAAACTTTGGGGAAGAGAAATCGACCCCTCAAACTCGAGAGATT	602	



XX WO200196547-A2.  
 XX 20-DEC-2001.  
 XX 14-JUN-2001; 2001WO-US019444.  
 XX 15-JUN-2000; 2000US-0212073P.  
 XX 23-JUN-2000; 2000US-0213467P.  
 XX 30-JUN-2000; 2000US-0215651P.  
 XX 07-JUL-2000; 2000US-0216605P.  
 XX 13-JUL-2000; 2000US-0218372P.  
 XX 25-AUG-2000; 2000US-0228056P.  
 XX (INCY-) INCYTE GENOMICS INC.  
 XX Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y;  
 PI Gandhi AR, Tribouley CM, Walia NK, Yao MG, Lu DAM, Greenwald SR;  
 PI Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang Y;  
 PI Paughn MG, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;  
 PI Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L;  
 PI Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;  
 XX WPI; 2002-090207/12.  
 DR P-PSDB; AAE16279.  
 XX New polypeptides, useful for diagnosing, treating or preventing disorders  
 of growth and development, cardiovascular and lipid, and diseases such as  
 cancer, comprise human kinase polypeptides.  
 XX Claim 5; Page 196; 197pp; English.  
 XX The invention relates to human kinase PKIN proteins and their  
 CC corresponding cDNAs. A composition containing PKIN agonist is useful for  
 CC treating a disease or condition associated with decreased expression of  
 CC PKIN and a composition comprising PKIN antagonist is useful for treating  
 CC a disease or condition associated with overexpression of PKIN. The  
 CC disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma,  
 CC myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder  
 CC (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease,  
 CC atherosclerosis, anaemia, allergies, adult respiratory distress syndrome,  
 CC autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes  
 CC mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease,  
 CC osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,  
 CC rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,  
 CC bacterial parasitic, fungal, viral, protozoal and helminthic infections)  
 CC growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,  
 CC Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio  
 CC vascular disease (arteriovenous fistula, hypertension, vasculitis,  
 CC aneurysms, congestive heart failure, angina pectoris, myocarditis,  
 CC ischaemic heart disease, chronic bronchitis, lung tumours); lipid  
 CC disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,  
 CC hypcholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity  
 CC of a test compound and in gene therapy. The present sequence is human  
 CC PKIN-25 cDNA  
 XX  
 XX Sequence 995 BP; 255 A; 295 C; 253 G; 192 T; 0 U; 0 Other;  
 SQ  
 Query Match 60.3%; Score 868; DB 6; Length 995;  
 Best Local Similarity 100.0%; Pred. No. 7e-216;  
 Matches 868; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 573 CTTTGATCGCCACCGGATCTGAATCCAGAACCGTCTCATGTGCCAGAGGACATCTC 632  
 DB 3 CTTTGATCGCCACCGGATCTGAATCCAGAACCGTCTCATGTGCCAGAGGACATCTC 62  
 QY 633 AGAGCTGGAGACGGCTCAGAACTCTGGAGTATCATAGGAACATGTCAGGGTCATTCC 692  
 DB 63 AGAGCTGGAGACGGCTCAGAACTCTGGAGTATCATAGGAACATGTCAGGGTCATTCC 122  
 QY 693 CTCCTACCCCAAAATCCTCAAGTTCATCAGTGTGACCGCCATGTGTGGAGTCTCTA 752  
 DB 123 CTCCTACCCCAAAATCCTCAAGTTCATCAGTGTGACCGCCATGTGTGGAGTCTCTA 192

QY 753 CCAGGCTCTGACCTATGTGTCAAAGCAACCATCGTACTAATGCCCGCTTACCCTCCAGGGT 812  
 DB 183 CCAGGCTCTGACCTATGTGTCAAAGCAACCATCGTACTAATGCCCGCTTACCCTCCAGGGT 242  
 QY 813 GCTGCTGCTGGGCTGTGGGAGTGGGAGGAGTCTGAGGCGCCCTCTCTGCGCCAGAA 872  
 DB 243 GCTGCTGCTGGGCTGTGGGAGTGGGAGGAGTCTGAGGCGCCCTCTCTGCGCCAGAA 302  
 QY 873 ATACAGGCTTGTCAATGTCTGTGGGCACTGCTGAAGAGGCTTGTGSCAGATAGGAC 932  
 DB 303 ATACAGGCTTGTCAATGTCTGTGGGCACTGCTGAAGAGGCTTGTGSCAGATAGGAC 362  
 QY 933 CACGTTTGGGAGCTCATCGAGCCCTCTTTGAAAGAGAGATGGCAGTTCCTGACAGCT 992  
 DB 363 CACGTTTGGGAGCTCATCGAGCCCTCTTTGAAAGAGAGATGGCAGTTCCTGACAGCT 422  
 QY 993 CCTCATGAAGGTGTGAGCGAGCGCTGGACAGAGCTGTCATCCAGAAAGCTGGGT 1052  
 DB 423 CCTCATGAAGGTGTGAGCGAGCGCTGGACAGAGCTGTCATCCAGAAAGCTGGGT 482  
 QY 1053 GCTACAGGGCTTCCCGGGGACCTCGACAGGCACTGCTGAACCGCTGGGCTTACAA 1112  
 DB 483 GCTACAGGGCTTCCCGGGGACCTCGACAGGCACTGCTGAACCGCTGGGCTTACAA 542  
 QY 1113 TCCCAACAGGGTGTGTTTCTGAAATGTCCTTGTGATTCCTGATTCATGAGGGCTGACTCT 1172  
 DB 543 TCCCAACAGGGTGTGTTTCTGAAATGTCCTTGTGATTCCTGATTCATGAGGGCTGACTCT 602  
 QY 1173 GAGAAGATTCATGATTCAGTCACTGGGGAAGGTACAACCTCATGTATACAGCCACTCCAC 1232  
 DB 603 GAGAAGATTCATGATTCAGTCACTGGGGAAGGTACACCTCATGTATACAGCCACTCCAC 662  
 QY 1233 CATGGAGATCCAGGCTCGGCTCTCTCAGAACCCAAAGGATGCTGAAGAGCAGGTCAAGCT 1292  
 DB 663 CATGGAGATCCAGGCTCGGCTCTCTCAGAACCCAAAGGATGCTGAAGAGCAGGTCAAGCT 722  
 QY 1293 GAAATGGACCTGTTCTACAGGAATCTCAGCTGACTTCGAGCAGTGTGTATGGTTCGGCCAT 1352  
 DB 723 GAAATGGACCTGTTCTACAGGAATCTCAGCTGACTTCGAGCAGTGTGTATGGTTCGGCCAT 782  
 QY 1353 CACCTCAATGGGACCGAGGACCCATACAGAGTCTTCGATATCATGAGAGTGGATCAT 1412  
 DB 783 CACCTCAATGGGACCGAGGACCCATACAGAGTCTTCGATATCATGAGAGTGGATCAT 842  
 QY 1413 TAATCCCTGTCGCCAAGAAATCCCTGA 1440  
 DB 843 TAATCCCTGTCGCCAAGAAATCCCTGA 870  
 RESULT 12  
 AAI58051  
 ID AAI58051 standard; cDNA; 1778 BP.  
 XX  
 AC AAI58051;  
 XX  
 DT 22-OCT-2001 (first entry)  
 XX  
 DE Human polynucleotide SEQ ID NO 254.  
 XX  
 KW Human; neotropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200153312-A1.  
 XX  
 XX 26-JUL-2001.  
 XX



PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
PI Zhou P, Goodrich R, Drmanac RT;  
XX WPI; 2001-442253/47.  
DR P-PSDB; AAM40681.

XX Novel nucleic acids and polypeptides, useful for treating disorders such  
PT as central nervous system injuries.

XX Claim 1; SEQ ID NO 3826; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the  
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localised neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activities, chemotactic/chemokinetic activity, haemostatic  
CC Activin/inhibin activity, cancer diagnosis and therapy, drug screening,  
CC and thrombolytic activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders. Note: The sequence data for this patent did not form  
CC part of the printed specification

XX SQ Sequence 721 BP; 178 A; 212 C; 188 G; 143 T; 0 U; 0 Other;

Query Match 43.0%; Score 619; DB 4; Length 721;

Best Local Similarity 100.0%; Pred. No. 5.46-151;

Matches 619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 GCAATGGCTCTGCAAAACATCTGAACAGCAGTCTCTCACTGGAGAACCTGATCTTA 279  
DB 103 GCAATGGCTCTGCAAAACATCTGAACAGCAGTCTCTCACTGGAGAACCTGATCTTA 162  
QY 280 AATGAGTTTCTTATACGGCCACCGAAGCCGAGAGGCTTTATCTGCAAGGAGACAGTT 339  
DB 163 AATGAGTTTCTTATACGGCCACCGAAGCCGAGAGGCTTTATCTGCAAGGAGACAGTT 222  
QY 340 CCCAGCGGCTGCTGCTGAGTTCAGGAGCCGCTGAGGAGGATTCATCAAG 399  
DB 223 CCCAGCGGCTGCTGCTGAGTTCAGGAGCCGCTGAGGAGGATTCATCAAG 282  
QY 400 CAGGCTGGATTTGGATGGCATTCCTGAGAGCGGTGAGAGGCTCTGAGGATCCAGACC 459  
DB 283 CAGGCTGGATTTGGATGGCATTCCTGAGAGCGGTGAGAGGCTCTGAGGATCCAGACC 342  
QY 460 CTGGGGATCACACCCAGACACGTCATTGTGCTGAGTGTCTCCAGACAGGCTCTGATCCAG 519  
DB 343 CTGGGGATCACACCCAGACACGTCATTGTGCTGAGTGTCTCCAGACAGGCTCTGATCCAG 402  
QY 520 AGAACTTGGGAGAGATTCAGACCTCAAACTGGAGATTTATCACACCCCTTCAC 579  
DB 403 AGAACTTGGGAGAGATTCAGACCTCAAACTGGAGATTTATCACACCCCTTCAC 462  
QY 580 TGGCCACCGAATTCGAATTCAGAACCGTCTCATGTGCGCAGAGACATCTCAGAGCTG 639  
DB 463 TGGCCACCGAATTCGAATTCAGAACCGTCTCATGTGCGCAGAGACATCTCAGAGCTG 522  
QY 640 GAGACGCTCAGAAAATCTGGAGTATCATAGGAACATCTGAGGGTCAATTCCTCTCTAC 699  
DB 523 GAGACGCTCAGAAAATCTGGAGTATCATAGGAACATCTGAGGGTCAATTCCTCTCTAC 582  
QY 700 CCCAAATCTCAAAGTCAATCAGTGTGCTGACCCAGCATGTGTGACCTCTTCTACAGCT 759  
DB 583 CCCAAATCTCAAAGTCAATCAGTGTGCTGACCCAGCATGTGTGACCTCTTCTACAGCT 642  
QY 760 CTGACCTATCTCAAAGCAACCATCTGATTAATGCCCGTTACCCGAGGCTGCTGCTG 819  
DB 643 CTGACCTATCTCAAAGCAACCATCTGATTAATGCCCGTTACCCGAGGCTGCTGCTG 702

QY 820 CTCGGGCTGTGGCAGTG 838  
DB 703 CTCGGGCTGTGGCAGTG 721

RESULT 14

ABK71537

ID ABK71537 standard; cDNA; 615 BP.

XX AC ABK71537;

XX DT 30-JUL-2002 (first entry)

XX DE Human dithp polynucleotide #3.

XX KW Human; dithp; diagnostic and therapeutic polynucleotide; gene; ss; bone;  
KW cell proliferative disorder; cancer; tumour; autoimmune disorder; brain;  
KW inflammatory disorder; viral infection; bacterial infection; seizure;  
KW fungal infection; parasitic infections; neurological disorder; breast;  
KW endocrine disorder; metabolic disorder; transport disorder; cervix;  
KW gastrointestinal disorder; transport disorder; gene therapy; kidney;  
KW adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;  
KW skin; testis; thymus.

XX OS Homo sapiens.

XX PN WO200220754-A2.

XX PD 14-MAR-2002.

XX PF 29-AUG-2001; 2001WO-US027127.

XX PR 05-SEP-2000; 2000US-0229747P.

XX PR 05-SEP-2000; 2000US-0229748P.

XX PR 05-SEP-2000; 2000US-0229749P.

XX PR 05-SEP-2000; 2000US-0229750P.

XX PR 05-SEP-2000; 2000US-0229751P.

XX PR 05-SEP-2000; 2000US-0230583P.

XX PR 06-SEP-2000; 2000US-0230583P.

XX PR 06-SEP-2000; 2000US-0230514P.

XX PR 06-SEP-2000; 2000US-0230515P.

XX PR 06-SEP-2000; 2000US-0230518P.

XX PR 06-SEP-2000; 2000US-0230519P.

XX PR 06-SEP-2000; 2000US-0230595P.

XX PR 06-SEP-2000; 2000US-0230597P.

XX PR 06-SEP-2000; 2000US-0230598P.

XX PR 06-SEP-2000; 2000US-0230599P.

XX PR 06-SEP-2000; 2000US-0230610P.

XX PR 06-SEP-2000; 2000US-0230865P.

XX PR 06-SEP-2000; 2000US-0230988P.

XX PR 07-SEP-2000; 2000US-0230989P.

XX PR 07-SEP-2000; 2000US-0231163P.

XX PR 07-SEP-2000; 2000US-0231167P.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL;

PI Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR;

PI Moniyama MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM;

PI Gerstlin EH, Peralta CH, David MH, Panzer SR, Flores V, Daffo A;

PI Marwaha R, Chen AJ, Chang SC, Au AP, Imman RR;

XX WPI; 2002-383054/41.

DR P-PSDB; ABG59945.

XX An isolated polynucleotide useful in diagnostics and therapeutics.

XX Claim 1; Page 406; 686pp; English.

XX The invention relates to human diagnostic and therapeutic (dithp)

CC polynucleotides and their associated polypeptides (DITHP polypeptides).

CC The sequences of the invention are used in the treatment and diagnosis of  
CC cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers  
CC (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast,  
CC cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or  
CC thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis,  
CC psoriasis, osteoporosis), viral infections, bacterial infections, fungal  
CC infections, parasitic infections, developmental disorders (e.g. anaemia,  
CC epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida),  
CC endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders  
CC (e.g. obesity, diabetes), neurological disorders (e.g. stroke,  
CC amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal  
CC disorders (e.g. ulcerative colitis, lymphoma) and transport disorders  
CC (e.g. myotonic dystrophy, cataract, peripheral neuropathy). Sequences  
CC ABK71535-ABK71809 represent human dithp polynucleotides of the invention  
XX  
SQ Sequence 615 BP; 165 A; 181 C; 153 G; 116 T; 0 U; 0 Other;  
  
Query Match 39.9%; Score 574; DB 6; Length 615;  
Best Local Similarity 99.7%; Pred. No. 2.8e-139;  
Matches 596; Conservative 0; Mismatches 0; Indels 2; Gaps 2;  
  
Qy 1 ATGAGCCGCACT-ATCGCCCGCAGCAGTATCCCGCCGAGATGCCCGAGTACGGGAGGA 59  
Db 18 ATGAGCCGCACTAATCGCCCGCAGCAGTATCCCGCCGAGATGCCCGAGTACGGGAGGA 77  
  
Qy 60 GAACCAATCTTCGAGTTGATGAGAGACATGCTGGAGCAACTCTGTATCCACCGAGCGGA 119  
Db 78 GAACCAATCTTCGAGTTGATGAGAGACATGCTGGAGCAACTCTGTATCCACCGAGCGGA 137  
  
Qy 120 AGATCCCATCCCTTCATGATCCAGCATCTGCATAGAGACAGCAATGTGCCAGGAT 179  
Db 138 AGATCCCATCCCTTCATGATCCAGCATCTGCATAGAGACAGCAATGTGCCAGGAT 197  
  
Qy 180 TGTATATTAGTCTCCACCGCTCAGCGGAAACAAACAATA-GCAATGTGGCTCTGCAAAAC 238  
Db 198 TGTATATTAGTCTCCACCGCTCAGCGGAAACAAACAATAAGGCAATGTGGCTCTGCAAAAC 257  
  
Qy 239 ATCTGAACAGCAGTCTCTCTACCCCTGGAGAACCTGTATTAATGAGTTTCTTATACGG 298  
Db 258 ATCTGAACAGCAGTCTCTCTACCCCTGGAGAACCTGTATTAATGAGTTTCTTATACGG 317  
  
Qy 299 CCACCGAAGCCAGAGGCTTTATCTGCAAGGAGACAGTTCCAGCGCGCTGCTCTCC 358  
Db 318 CCACCGAAGCCAGAGGCTTTATCTGCAAGGAGACAGTTCCAGCGCGCTGCTCTCC 377  
  
Qy 359 AGCTGATTTCAGAACCGCTGCTGCTGAAGAGGATTCATCAAGCAGGCTGGATTCGGATG 418  
Db 378 AGCTGATTTCAGAACCGCTGCTGCTGAAGAGGATTCATCAAGCAGGCTGGATTCGGATG 437  
  
Qy 419 GCATCCCTGAGACGCGTGAGCAGGCTCTGAGGATCCAGACCTTGGGATCACCCAGAC 478  
Db 438 GCATCCCTGAGACGCGTGAGCAGGCTCTGAGGATCCAGACCTTGGGATCACCCAGAC 497  
  
Qy 479 AGCTCATTTGCTGAGTCTCCAGACGCTTCTGATCGAGAGAACTTGGGGAGAGAA 538  
Db 498 AGCTCATTTGCTGAGTCTCCAGACGCTTCTGATCGAGAGAACTTGGGGAGAGAA 557  
  
Qy 539 TCGACCTTCAAACTGGAGAGATTTATCACACCACTTTGATGGCCACCCGAAATCTGA 596  
Db 558 TCGACCTTCAAACTGGAGAGATTTATCACACCACTTTGATGGCCACCCGAAATCTGA 615  
  
RESULT 15  
ID AAK51550  
XX AAK51550 standard; cDNA; 997 BP.  
XX AAK51550;  
XX  
XX 06-NOV-2001 (first entry)  
XX Human polynucleotide SEQ ID NO 95.  
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;

KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
KW nervous system disorder; arthritis; inflammation; ss.  
OS Homo sapiens.  
XX WO200157190-A2.  
PN 09-AUG-2001.  
XX 05-FEB-2001; 2001WO-US004098.  
XX 03-FEB-2000; 2000US-00496914.  
PR 27-APR-2000; 2000US-00560875.  
PR 20-JUN-2000; 2000US-00598075.  
PR 19-JUL-2000; 2000US-00620325.  
PR 01-SEP-2000; 2000US-00654936.  
PR 15-SEP-2000; 2000US-00663561.  
PR 20-OCT-2000; 2000US-00693325.  
PR 30-NOV-2000; 2000US-00728422.  
XX (HYSE-) HYSEQ INC.  
PA Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;  
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;  
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;  
XX WPI; 2001-476283/51.  
DR P-PSDB; AAM78417.  
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful  
XX in diagnosis and gene therapy.  
XX Claim 1; Page 714-715; 6221pp; English.  
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the  
XX encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to  
XX cytokine, cell proliferation or cell differentiation or which may induce  
XX production of other cytokines in other cell populations. The  
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or  
XX peptide therapy. The polypeptides have various cytokine-like activities,  
XX e.g. stem cell growth factor activity, haematopoiesis regulating  
XX activity, tissue growth factor activity, immunomodulatory activity and/or  
XX activin/inhibin activity and may be useful in the diagnosis and/or  
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and  
XX inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111  
XX (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the  
XX sequence listing were missing at the time of publication  
SQ Sequence 997 BP; 253 A; 279 C; 282 G; 183 T; 0 U; 0 Other;  
  
Query Match 32.2%; Score 463.4; DB 4; Length 997;  
Best Local Similarity 99.8%; Pred. No. 2.4e-110;  
Matches 464; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 976 GCAGTTCTTGACAGCTCTCTCATGAAGGTGCTGAGCAGCGCTGACAGGAGTGC 1035  
Db 407 GTAGTTCTTGACAGCTCTCTCATGAAGGTGCTGAGCAGCGCTGACAGGAGTGC 466  
  
Qy 1036 ATCCAGAAAGGTGGGTGTACACGGGTCCTCCGGGACCTCGACAGGACACCTGCTG 1095  
Db 467 ATCCAGAAAGGTGGGTGTACACGGGTCCTCCGGGACCTCGACAGGACACCTGCTG 526  
  
Qy 1096 AACGGCTGGGTGTACATCCACAGGCTGTTTTCTGAATGTGCAATTGATTCATC 1155  
Db 527 AACGGCTGGGTGTACATCCACAGGCTGTTTTCTGAATGTGCAATTGATTCATC 586  
  
Qy 1156 ATGAGCGGCTGACTCTTGAGAGAAATTTGATCCAGTCACTGGGAAAGGTACCACTCATG 1215  
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Qy 1216 TACAGCCACTTCCACCATGGAGATCCAGGCTCGCTCTGAGAACCCAAAGGATGCT 1275

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Db      647 TACAAGCCACCTCCACCACATGGAGATCCAGCTCGCTCTCTGAGAACCCAAAGGATGCT 706
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QY      1336 TTGTATGGGTTCGGCCATCACCCCTCAATGGGACGAGGCCCATACACAGTCTTCGAATAC 1395
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QY      1396 ATCGAGAGTGGGATCATTATCCCTGCCCAAGAAAATCCCTGA 1440
Db      827 ATCGAGAGTGGGATCATTATCCCTGCCCAAGAAAATCCCTGA 871

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Search completed: March 19, 2005, 20:53:48  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 19, 2005, 19:37:19 ; Search time 6103 Seconds  
(without alignments)  
11432.986 Million cell updates/sec

Title: US-10-798-773-1  
Perfect score: 1440  
Sequence: 1 atggagccactatcgcccc.....tgcccaagaataccccctga 1440

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: GenEmbl.\*
- 2: gb.ba.\*
- 3: gb.hcg.\*
- 4: gb.in.\*
- 5: gb.om.\*
- 6: gb.ov.\*
- 7: gb.pat.\*
- 8: gb.ph.\*
- 9: gb.pl.\*
- 10: gb.pr.\*
- 11: gb.ro.\*
- 12: gb.sts.\*
- 13: gb.sy.\*
- 14: gb.un.\*
- 15: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1440	100.0	1579	6	AX714697 Sequence
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4	1440	100.0	1656	9	BC034776 Homo sapi
5	1440	100.0	2185	9	BC050576 Homo sapi
6	1170	81.2	1619	6	AX748132 Sequence
7	1170	81.2	1619	6	AK093446 Homo sapi
8	1032.8	71.7	1452	6	AX211563 Sequence
9	928	64.4	1581	10	BC079446 Rattus no
10	868	60.3	995	6	AX642974 Sequence
11	759.8	52.8	774	6	AX211565 Sequence
12	577	40.1	577	6	CQ724754 Sequence
13	574	39.9	615	6	AX721043 Sequence
14	553.8	38.5	1674	5	BC062516 Xenopus t
15	319	22.2	1608	6	CQ734872 Sequence
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17	285	19.8	285	6	AR534561 Sequence
18	240	16.7	45437	2	AC002095 Homo sapi
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28	149.6	10.4	662	3	AK114674 Ciona int
29	147	10.2	44266	9	AC000392 Genomic s
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c	139	9.7	264638	2	AC129847 Rattus no
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ALIGNMENTS

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LOCUS AR534560 Sequence 1 from patent US 6734010.  
DEFINITION AR534560 1440 bp DNA linear PAT 08-OCT-2004  
ACCESSION AR534560  
VERSION AR534560.1 GI:53924889  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1440)  
AUTHORS Yu.X., Xie.Q., Abuin.A. and Walke.D.W.  
TITLE Human kinases and polynucleotides encoding the same  
JOURNAL Patent: US 6734010-A 1 11-MAY-2004;  
FEATURES  
Location/Qualifiers  
source 1. 1440  
/mol\_type="genomic DNA"

Query Match	Best Local Similarity	Score	DB	Length
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QY	61	AACACATCTTCGAGTTGATGAGAACATCTCTGGAGCACTCTCTGATCCACAGCCGAA	120	
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Db	181	GTAATATTAGTCCACCGCTCAGGAGAAACAAATAGCAATGTGGCTCTGCACAAAT	240	
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RESULT 2  
AX714697 1579 bp DNA linear PAT 15-APR-2003  
LOCUS Sequence 1381 from Patent EP1293569.  
DEFINITION AX714697  
ACCESSION AX714697  
VERSION AX714697.1 GI:29889650  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Tsogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S., Yamamoto, J.I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R., Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and Masuho, Y.  
TITLE Full-length cDNAs  
JOURNAL Patent: EP 1293569-A 1381 19-MAR-2003;  
Helix Research Institute (JP); Research Association for Biotechnology (JP)  
FEATURES  
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 AACCAATCTTCAGTTGATGACAGAACTGCTGGAGCACTCTGATCCACGAGCCGAA 120  
Db 90 AACCAATCTTCAGTTGATGACAGAACTGCTGGAGCACTCTGATCCACGAGCCGAA 149  
Qy 121 GATCCCATCCCTTCATGATCCAGCATTTGCAATGAGACAACTGTCAGGATTT 180  
Db 150 GATCCCATCCCTTCATGATCCAGCATTTGCAATGAGACAACTGTCAGGATTT 209  
Qy 181 GTAATATAGTCCACCGCTCAGGAGAAACAACTAGCAATGAGCTCTGCAACAT 240  
Db 210 GTAATATAGTCCACCGCTCAGGAGAAACAACTAGCAATGAGCTCTGCAACAT 269  
Qy 241 CTGAACAGCAGTCTCTTACCTGAGGAACTGATCTTAATGAGTTTCTTACGGCC 300  
Db 270 CTGAACAGCAGTCTCTTACCTGAGGAACTGATCTTAATGAGTTTCTTACGGCC 329  
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## RESULT 3

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LOCUS AK057266 1579 bp mRNA linear PRI 30-JAN-2004  
DEFINITION Homo sapiens cDNA FLJ32704 f15, clone TEST12000591, weakly similar  
to ADENYLATE KINASE, CHLOROPLAST (EC 2.7.4.3).  
ACCESSION AK057266  
VERSION AK057266.1 GI:16552887  
KEYWORDS oligo capping; f15 (full insert sequence).  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS

1 Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Oobayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahara, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Hirakawa, S., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiyosaka, K., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Sakaki, N., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togaishi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, K., Nakai, K., Yada, I., Nakamura, Y., Ohara, O., Isogai, T., and Sugano, S. Complete sequencing and characterization of 21,243 full-length human cDNAs  
Nat. Genet. 36 (1), 40-45 (2004)

## TITLE

JOURNAL  
PUBMEDREFERENCE  
AUTHORS

2 Ishibashi, T., Kanehori, K., Yosida, M., Watanabe, S., Ishida, S., Ono, Y., Hotuta, T., Hiraoka, S., Murakawa, K., Takiguchi, S., Kusano, J., Watanabe, M., Fujimori, K., Tanai, H., Ishida, M., Yamashita, H., Chiba, Y., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahara, K., Masuho, Y., Nagai, K., and Isogai, T. NEDO human cDNA sequencing project  
Unpublished  
3 (bases 1 to 1579)  
Isogai, T., Otsuki, T. and Sugiyama, T. Direct Submission  
Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)  
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5' & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and HRI.

TITLE  
JOURNALREFERENCE  
AUTHORS

## JOURNAL

## COMMENT

## FEATURES

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## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
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## RESULT 4

BC034776

LOCUS

DEFINITION

Homo sapiens chromosome 9 open reading frame 98, mRNA (cdna clone

MGC:35281 IMAGE:5175757), complete cds.

BC034776

VERSION

BC034776.1

KEYWORDS

MGC.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1656)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,

Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,

Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,

Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,

Scapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,

Sheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,

Carninci,P., Prange,C., Raja,S.S., Loquellano,N.A., Peters,G.J.,

Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,

McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,

Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,

Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,

Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,

Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,

Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,

Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,

Butterfield,Y.S., Krzywinski,M.I., Skalek,U., Smallos,D.E.,

Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cdna sequences

TITLE

JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 1656)  
Strausberg, R.  
Direct Submission  
Submitted (24-JUL-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome  
Sequencing Center  
Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lounseged, H.,  
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,  
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAC Plate: 51 Row: 1 Column: 3  
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## ORIGIN

Query Match 100.0%; Score 1440; DB 9; Length 1656;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACGCCCATATCGCCCGCACCGTATCCCCCGGAGATGCCAGTAGTCGGGAGGAG 60  
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DEFINITION Homo sapiens chromosome 9 open reading frame 98, mRNA (cDNA clone
MGC:57797 IMAGE:5744517), complete cds.
ACCESSION BC050576
VERSION BC050576.1 GI:30046787
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
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Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heideh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Schetz,T.E., Brownstein,M.J., Udwin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
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Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,B.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 2185)
Strausberg,R.
Direct Submission
Submitted (08-APR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-sbgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

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## RESULT 6

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LOCUS AX748132  
DEFINITION Sequence 1657 from Patent EP1308459.  
ACCESSION AX748132  
VERSION AX748132.1 GI:32132520  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1  
Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S.,  
Yamamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R.,  
Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and  
Masuho, Y.  
Full-length cDNA sequences  
Patent: EP 1308459-A 1657 07-MAY-2003;  
Helix Research Institute (JP); Research Association for  
Biotechnology (JP)  
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 ACCESSION AK093446  
 VERSION AK093446.1 GI:21752320  
 KEYWORDS oligo capping; fis (full insert sequence).  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Ohtsuka, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahara, K., Murakami, K., Yaeuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamiyama, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, T., Kusano, J., Kanehori, K., Takahashi, S., Watanabe, S., Hara, H., Tanase, T., Nomura, Y., Togiuchi, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Mueshino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Mori, S., Momiya, S., Momiya, H., Sato, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, P., Wakebe, H., Hishigaki, H., Watanabe, T.,

Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hiro, M., Ohmori, Y., Kawabata, A., Hiki, J., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.  
 Complete sequencing and characterization of 21,243 full-length human cDNAs  
 Nat. Genet. 36 (1), 40-45 (2004)  
 14702039  
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 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 PUBLISHED  
 Ishibashi, T., Kanehori, K., Yosida, M., Watanabe, S., Ishida, S., Ono, Y., Hotta, T., Hiraoka, S., Murakawa, K., Takiguchi, S., Kusano, J., Watanabe, M., Fujimori, K., Tanai, H., Ishida, M., Yamashita, H., Chiba, Y., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahara, K., Masuho, Y., Nagai, K. and Isogai, T.  
 NEDO human cDNA sequencing project  
 Unpublished  
 3 (bases 1 to 1619)  
 Direct Submission  
 Isogai, T. and Yamamoto, J.  
 TITLE  
 JOURNAL  
 PUBLISHED  
 COMMENT  
 Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan  
 (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)  
 NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.  
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 JOURNAL

REMARK  
 COMMENT

FEATURES  
 source

BC079446 1581 bp mRNA linear ROD 15-SEP-2004  
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 Rattus norvegicus (Norway rat)

Rattus norvegicus  
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

1 (bases 1 to 1581)  
 Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,  
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
 Hopkins, R.P., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,  
 Carninci, P., Brownstein, M.J., Bosak, S.A., McEwan, P.J.,  
 Abramson, K.J., Mullahy, S.J., Gunaratne, P.H., Richards, S.,  
 McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
 Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S.,  
 Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
 Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
 Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,  
 Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 12477932

2 (bases 1 to 1581)  
 Director MGC Project.  
 Direct Submission  
 Submitted (02-AUG-2004) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgabbs@mail.nih.gov](mailto:cgabbs@mail.nih.gov)

Tissue Procurement: Howard Jacobs  
 cDNA Library Preparation: Express Genomics  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 CDNA Sequencing by: Sequencing Group at the Stanford Human Genome  
 Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www.shgc.stanford.edu>  
 Contact: (Dickson, Mark) [mcdpaxil@stanford.edu](mailto:mcdpaxil@stanford.edu)  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
 R. M.

Clone distribution: MGC clone distribution information can be found  
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ORIGIN

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VERSION AX642974.1  
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ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1  
AUTHORS Yue,H., Lal,P., Bandman,O., Borowsky,M., Au-Young,J., Lu,Y.,  
Gandhi,A.R., Tribouley,C.M., Walla,N., Yao,M.G., Lu,D.A.,  
Greenwald,S.R., Ramkumar,J., Griffin,J.A., Kearney,L., Burford,N.,  
Nguyen,D.B., Tang,Y.T., Baughn,M.R., He,A., Thornton,M.,  
Hafalla,A., Patterson,C., Gururajan,R., Lo,T.P., Khan,F.,  
Recipon,S.A., Azimzai,Y., Policky,J.L., Ding,L., Grether,M.,  
Elliot,V.S., Thangavelu,K., Batra,S. and Ison,C.H.  
HUMAN KINASES  
TITLE Patent: WO 01096547-A 51 20-DEC-2001;  
JOURNAL Incyte Genomics, Inc. (US)  
FEATURES Location/Qualifiers  
source 1. 995

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AX211565
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VERSION CQ724754.1 GI:42285611  
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ORGANISM Homo sapiens  
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AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.  
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JOURNAL Patent: WO 02068579-A 10688 06-SEP-2002;  
PE Corporation (NY) (US)  
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DEFINITION Sequence 3 from Patent WO0220754.  
ACCESSION AX721043  
VERSION AX721043.1 GI:30421879  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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Lincoln, S.E., Altus, C.M., Dufour, G.E., Chalup, M.S., Hillman, J.L.,  
Jones, A., Yu, J.Y., Wright, R.J., Gietzen, D., Liu, Toomy, F., Yap, E.,  
Dani, C.R., Momiyama, M., Bradley, D., Kohatgi, S., Harris, B.,  
Roseberry, A.M., Gerstin, E.H., Peralta, C.H., David, M., Panzer, S.,  
Flores, V., Daffo, A., Marwaha, R., Chen, A., Chang, S.C. and Inman, R.R.  
TITLE Molecules for diagnostics and therapeutics  
JOURNAL Patent: WO 0220754-A 3 14-MAR-2002;  
Incyte Genomics, Inc. (US)  
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DEFINITION
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ACCESSION
  BC062516
VERSION
  BC062516.1 GI:38566161
KEYWORDS
  MGC.
SOURCE
  Xenopus tropicalis (Silurana tropicalis)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
  1 (bases 1 to 1674)
  Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
  Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
  Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
  Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
  Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
  Scapleton, T.E., Soares, M.B., Bonaldo, M.P., Casavant, T.L.,
  Scheetz, T.M., Brownstein, M.J., Uedin, T.B., Teohiyuki, S.,
  Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
  Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
  McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
  Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
  Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
  Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
  Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
  Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
  Butterfield, Y.S., Krzyzanski, M.I., Skalska, U., Smailus, D.E.,
  Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
  Generation and initial analysis of more than 15,000 full-length
  human and mouse cDNA sequences
  Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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  2 (bases 1 to 1674)
  Klein, S. and Gerhard, D.S.
  Direct Submission
  Submitted (17-NOV-2003) National Institutes of Health, Xenopus Gene
  Collection (XGC), National Institute of Child Health and Human
  Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD
  20892-7510, USA
  NTH-MGC Project
  Contact: XGC help desk
  Email: csapbs@mail.nih.gov
  Tissue Procurement: Robert M. Grainger
  cDNA Library Preparation: Life Technologies, Inc.
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Genome Sequence Centre,
  BC Cancer Agency, Vancouver, BC, Canada
  info@cgsc.bc.ca
  Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
  Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth
  Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
  Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
  Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
  Parvaneh Saeedi, JR Santos, Angélique Schnerch, Ursula Skalska,
  Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacque
  Schein, Asim Siddiqui, Rob Holt, Marco Marra.
  Clone distribution: MGC clone distribution information can be found
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  QY 121 GATCCCATCCCTTCATGATCCAGCACTTGCTATAGAGAACACACATGTCAGGATT 180
  DB 126 GACCAATCAGTACATGATGATGATCTCTCCAAATGATATGATGATGATGATGAT 185
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Search completed: March 19, 2005, 22:35:43  
Job time : 6115 secs

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VERSION CQ734872.1 GI:42324765  
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ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.  
TITLE Kits, such as nucleic acid arrays, comprising a majority of  
humanexons or transcripts, for detecting expression and other uses  
thereof  
JOURNAL Patent: WO 02068579-A 20806 06-SEP-2002;

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